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OM protein - protein search, using sw model

Run on: February 4, 2003, 12:56:41 ; Search time 15.4575 Seconds
(without alignments)
315.977 Million cell updates/sec

Title: US-09-854-864-15

Perfect score: 909
Sequence: 1 MSGGGRSRGGSRVDQER.....SPALPGKLADQVALVYST 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	909	100.0	166	US-08-810-572A-6	Sequence 6, Appli
2	909	100.0	166	US-09-290-333-6	Sequence 6, Appli
3	909	100.0	293	US-08-810-572A-2	Sequence 2, Appli
4	909	100.0	293	US-09-290-333-2	Sequence 2, Appli
5	82.5	9.1	799	US-08-525-940-23	Sequence 23, Appli
6	82.5	9.1	799	US-08-976-838-23	Sequence 23, Appli
7	82.5	9.1	881	US-08-525-940-21	Sequence 21, Appli
8	82.5	9.1	881	US-08-976-838-21	Sequence 21, Appli
9	82.5	9.1	915	US-08-525-940-18	Sequence 18, Appli
10	82.5	9.1	915	US-08-976-838-18	Sequence 18, Appli
11	82.5	9.1	915	US-09-214-555B-2	Sequence 2, Appli
12	82.5	9.1	915	US-09-214-555B-7	Sequence 7, Appli
13	81	8.9	704	US-09-590-656-2	Sequence 2, Appli
14	81	8.9	977	US-09-590-656-1	Sequence 1, Appli
15	81	8.9	1124	US-08-323-474-2	Sequence 2, Appli
16	81	8.9	1124	PCT-US93-06093-2	Sequence 2, Appli
17	79.5	8.7	98	US-08-465-380-21	Sequence 21, Appli
18	79.5	8.7	98	US-08-480-478-49	Sequence 49, Appli
19	79.5	8.7	98	US-08-486-397-21	Sequence 21, Appli
20	79.5	8.7	98	US-08-486-399-21	Sequence 21, Appli
21	79.5	8.7	98	US-08-461-965-21	Sequence 21, Appli
22	79.5	8.7	98	US-08-326-110A-49	Sequence 49, Appli
23	79.5	8.7	98	US-08-634-641-21	Sequence 21, Appli
24	79.5	8.7	98	US-09-249-471-21	Sequence 21, Appli
25	79.5	8.7	98	US-09-249-472-21	Sequence 21, Appli
26	79.5	8.7	98	US-09-249-451-21	Sequence 21, Appli
27	79.5	8.7	98	US-08-809-455-21	Sequence 21, Appli

28	79.5	8.7	98	US-09-249-461-21	Sequence 21, Appli
29	79.5	8.7	98	US-09-249-448-21	Sequence 21, Appli
30	78	8.6	518	US-08-385-229-4	Sequence 4, Appli
31	77.5	8.5	75	US-08-465-380-6	Sequence 6, Appli
32	77.5	8.5	75	US-08-465-380-41	Sequence 41, Appli
33	77.5	8.5	75	US-08-480-478-35	Sequence 35, Appli
34	77.5	8.5	75	US-08-486-397-6	Sequence 6, Appli
35	77.5	8.5	75	US-08-486-399-6	Sequence 6, Appli
36	77.5	8.5	75	US-08-486-399-41	Sequence 41, Appli
37	77.5	8.5	75	US-08-486-399-41	Sequence 41, Appli
38	77.5	8.5	75	US-08-461-965-6	Sequence 6, Appli
39	77.5	8.5	75	US-08-461-965-41	Sequence 41, Appli
40	77.5	8.5	75	US-08-326-110A-35	Sequence 35, Appli
41	77.5	8.5	75	US-08-634-641-6	Sequence 6, Appli
42	77.5	8.5	75	US-08-634-641-41	Sequence 41, Appli
43	77.5	8.5	75	US-09-249-471-6	Sequence 6, Appli
44	77.5	8.5	75	US-09-249-471-41	Sequence 41, Appli
45	77.5	8.5	75	US-09-249-472-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-810-572A-6
; Sequence 6, Application US/08810572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,572A
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-810-572A-6
Query Match 100.0%; Score 909; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-90;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGIGSRGRRGSRVDOERFPQGLMTGVAMRSCPEEQYMDPLGTGCMCKTICNHQSQR 60
DB 1 MSGIGSRGRRGSRVDOERFPQGLMTGVAMRSCPEEQYMDPLGTGCMCKTICNHQSQR 60

QY 61 TCAAFGRSLSCREKQGFYDHLRDCISGASICGHPKQCAVFCENKLRSPVNLPEELRR 120
DB 61 TCAAFGRSLSCREKQGFYDHLRDCISGASICGHPKQCAVFCENKLRSPVNLPEELRR 120

QY 121 QRSGEVENNSDNGRYQGLERHGRSEASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVENNSDNGRYQGLERHGRSEASPALPGLKLSADQVALVYST 166

RESULT 2
US-09-290-333-6
Sequence 6, Application US/09290333
Patent No. 6316222

GENERAL INFORMATION:
APPLICANT: Bram, Richard J.

von Bulow, Gotz

TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th

FLOOR

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/290,333

FILING DATE: 12-Apr-1999

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1340-1-007 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 166 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-290-333-6

Query Match 100.0%; Score 909; DB 4; Length 166;

Best Local Similarity 100.0%; Pred. No. 2e-90;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGIGSRGRRGSRVDOERFPQGLMTGVAMRSCPEEQYMDPLGTGCMCKTICNHQSQR 60

DB 1 MSGIGSRGRRGSRVDOERFPQGLMTGVAMRSCPEEQYMDPLGTGCMCKTICNHQSQR 60

QY 61 TCAAFGRSLSCREKQGFYDHLRDCISGASICGHPKQCAVFCENKLRSPVNLPEELRR 120

DB 61 TCAAFGRSLSCREKQGFYDHLRDCISGASICGHPKQCAVFCENKLRSPVNLPEELRR 120

QY 121 QRSGEVENNSDNGRYQGLERHGRSEASPALPGLKLSADQVALVYST 166

DB 121 QRSGEVENNSDNGRYQGLERHGRSEASPALPGLKLSADQVALVYST 166

RESULT 3
US-08-810-572A-2

Sequence 2, Application US/08810572A
Patent No. 5969102

GENERAL INFORMATION:

APPLICANT: Bram, Richard J.

von Bulow, Gotz

TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th

FLOOR

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/810,572A

FILING DATE: 28-FEB-1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1340-1-007

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 293 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

US-08-810-572A-2

Query Match 100.0%; Score 909; DB 2; Length 293;

Best Local Similarity 100.0%; Pred. No. 4e-90;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGIGSRGRRGSRVDOERFPQGLMTGVAMRSCPEEQYMDPLGTGCMCKTICNHQSQR 60

DB 1 MSGIGSRGRRGSRVDOERFPQGLMTGVAMRSCPEEQYMDPLGTGCMCKTICNHQSQR 60

QY 61 TCAAFGRSLSCREKQGFYDHLRDCISGASICGHPKQCAVFCENKLRSPVNLPEELRR 120

DB 61 TCAAFGRSLSCREKQGFYDHLRDCISGASICGHPKQCAVFCENKLRSPVNLPEELRR 120

QY 121 QRSGEVENNSDNGRYQGLERHGRSEASPALPGLKLSADQVALVYST 166

DB 121 QRSGEVENNSDNGRYQGLERHGRSEASPALPGLKLSADQVALVYST 166

RESULT 4
US-09-290-333-2
Sequence 2, Application US/09290333
Patent No. 6316222
GENERAL INFORMATION:
APPLICANT: Bratt, Richard J.
VON BULOW, Goltz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAMEL, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/290,333
FILING DATE: 12-Apr-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEITICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-290-333-2
Query Match
Best Local Similarity 100.0%; Score 909; DB 4; Length 293;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGIGSRGRGRSRVDOERPPQGIWTVAMRSCPEEQYMDPLIGTSCSKTICNHQSQR 60
DB 1 MSGIGSRGRGRSRVDOERPPQGIWTVAMRSCPEEQYMDPLIGTSCSKTICNHQSQR 60
QY 61 TCAPFCRSLCRKCKGKYDHLRDCISCASTCGHPKQCAFECNKLRSPNLPPELRR 120
DB 61 TCAPFCRSLCRKCKGKYDHLRDCISCASTCGHPKQCAFECNKLRSPNLPPELRR 120
QY 121 QRSGEVENNSDNGSGRYQGLERHGSASPALPGLKLSADQVALVYST 166
DB 121 QRSGEVENNSDNGSGRYQGLERHGSASPALPGLKLSADQVALVYST 166

RESULT 5
US-08-525-940-23
Sequence 23, Application US/08525940
Patent No. 5866351
GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
APPLICANT: Miranda, Luis R.

APPLICANT: Wolf, Joseph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES AND GENES
TITLE OF INVENTION: ENCODING SAID PROTEASES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,940
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,852
FILING DATE: 01-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/088,322
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-525-940-23
Query Match
Best Local Similarity 9.1%; Score 82.5; DB 2; Length 799;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;

QY 27 TGVAMRSCPEEQYMDPLIGTSCSKTICNHQSORTCAF-----CR-----SLSC 71
DB 603 TNSCVTHCPDGSYQDPTKKNLCRKCSENC-----XTCTEFHNCTECRDGLSLQGSRCVSVC 657
QY 72 RKEQKFFYDHLRDCISCASTCGHPKQCF-----AYPCEN 106
DB 658 --EDGRYFNG--QDQPCRHRCATCAGAGADGCTNCTEGTFMED 657

RESULT 6
US-08-976-838-23
Sequence 23, Application US/08976838
Patent No. 5981259
GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASE NUCLEIC ACID
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,838
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-976-838-23

Query Match 9.1%; Score 82.5; DB 2; Length 799;
Best Local Similarity 26.0%; Pred. No. 1.5;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;

Qy 27 TGVAMRSCPEEQYMDPLGTGCMSCKTICNHQSQRTCAAF-----CR-----SLSC 71
Db 603 TNSCVTHCPDGSYQDTKXNLCRKCSENC-----KTCTEFHNCTEGRDGLSLQSRCSVSC 657
Qy 72 RKEQGFYDHLRDCISCSAIC---GQHPKQC---AYFCEN 106
Db 658 --EDGRYFNG--QDCQPCHRFCATCAGAGADGCINCTEGYFME 697

RESULT 7

US-08-525-940-21
Sequence 21, Application US/08525940
Patent No. 5866351
GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
APPLICANT: Miranda, Luis R.
APPLICANT: Wolf, Joseph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES AND GENES
TITLE OF INVENTION: ENCODING SAID PROTEASES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSES: Sheridan Rose & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,940
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,852
FILING DATE: 01-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/088,322
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700

TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 881 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-525-940-21

Query Match 9.1%; Score 82.5; DB 2; Length 881;
Best Local Similarity 26.0%; Pred. No. 1.7;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;

Qy 27 TGVAMRSCPEEQYMDPLGTGCMSCKTICNHQSQRTCAAF-----CR-----SLSC 71
Db 685 TNSCVTHCPDGSYQDTKXNLCRKCSENC-----KTCTEFHNCTEGRDGLSLQSRCSVSC 739
Qy 72 RKEQGFYDHLRDCISCSAIC---GQHPKQC---AYFCEN 106
Db 740 --EDGRYFNG--QDCQPCHRFCATCAGAGADGCINCTEGYFME 779

RESULT 8

US-08-976-838-21
Sequence 21, Application US/08976838
Patent No. 5981259
GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASE NUCLEIC ACID
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSES: Sheridan Rose P.C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,838
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 881 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-976-838-21

Query Match 9.1%; Score 82.5; DB 2; Length 881;
Best Local Similarity 26.0%; Pred. No. 1.7;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;

Qy 27 TGVAMRSCPEEQYMDPLGTGCMSCKTICNHQSQRTCAAF-----CR-----SLSC 71
Db 685 TNSCVTHCPDGSYQDTKXNLCRKCSENC-----KTCTEFHNCTEGRDGLSLQSRCSVSC 739
Qy 72 RKEQGFYDHLRDCISCSAIC---GQHPKQC---AYFCEN 106
Db 740 --EDGRYFNG--QDCQPCHRFCATCAGAGADGCINCTEGYFME 779

RESULT 9
US-08-525-940-18
Sequence 18, Application US/08525940
Patent No. 5866351
GENERAL INFORMATION:
APPLICANT: Franzsoff, Alex
APPLICANT: Miranda, Luis R.
APPLICANT: Wolf, Joseph R.
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASES AND GENES
TITLE OF INVENTION: ENCODING SAID PROTEASES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
City: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,940
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,852
FILING DATE: 01 JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/088,322
FILING DATE: 07 JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 915 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-525-940-18
Query Match 9.1%; Score 82.5; DB 2; Length 915;
Best Local Similarity 26.0%; Pred. No. 1.8;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;
QY 27 TGVAMRSCPEBQYMDPLIGTMSCKTICNHOSORTCAAF-----CR-----SLSC 71
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QY 72 RKEQGKFDHLRDLICASCASIC---GQHPKQC-----AYPCEN 106
DB 774 --EDGRYFNG--QDCQPCRFRCATCAGAGADGCTNCTEGYFME 813
RESULT 10
US-08-976-838-18
Sequence 18, Application US/08976838
Patent No. 5981259
GENERAL INFORMATION:
APPLICANT: Franzsoff, Alex
TITLE OF INVENTION: CD4+ T-LYMPHOCYTE PROTEASE NUCLEIC ACID
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:

ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
City: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,838
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-11-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 915 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-976-838-18
Query Match 9.1%; Score 82.5; DB 2; Length 915;
Best Local Similarity 26.0%; Pred. No. 1.8;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;
QY 27 TGVAMRSCPEBQYMDPLIGTMSCKTICNHOSORTCAAF-----CR-----SLSC 71
DB 719 TNSCVTHCPDGSYDPTKKNLCRKSENC-----KTCTEFHNCTEGRDGLSLQGRCSVSC 773
QY 72 RKEQGKFDHLRDLICASCASIC---GQHPKQC-----AYPCEN 106
DB 774 --EDGRYFNG--QDCQPCRFRCATCAGAGADGCTNCTEGYFME 813
RESULT 11
US-09-214-555B-2
Sequence 2, Application US/09214555B
Patent No. 6380171
GENERAL INFORMATION:
APPLICANT: INSTITUT DE RECHERCHE CLINIQUE DE MONTREAL
TITLE OF INVENTION: PRO-PROTEIN CONVERTING ENZYME
FILE REFERENCE: PRO-PROTEIN CONVERT ENZ
CURRENT APPLICATION NUMBER: US/09/214,555B
CURRENT FILING DATE: 1999-01-04
PRIOR APPLICATION NUMBER: 60/021,008
PRIOR FILING DATE: 1996-07-26
PRIOR APPLICATION NUMBER: 2,203,745
PRIOR FILING DATE: 1997-04-25
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 2
LENGTH: 915
TYPE: PRT
ORGANISM: Homo sapiens
US-09-214-555B-2
Query Match 9.1%; Score 82.5; DB 4; Length 915;
Best Local Similarity 26.0%; Pred. No. 1.8;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;
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DB 719 TNSCVTHCPDGSYDPTKKNLCRKSENC-----KTCTEFHNCTEGRDGLSLQGRCSVSC 773

Qy 72 RKEQKFDHLRDLCTSCASIC-----GQHPKOC-----AYFCEN 106
Db 774 --EDGRYFNG--QDCOPCHRFATCATGAGADGACINCTEGYFMD 813

RESULT 12

US-09-214-555B-7
; Sequence 7, Application US/09214555B
; Patent No. 6380171
; GENERAL INFORMATION:
; APPLICANT: INSTITUT DE RECHERCHE CLINIQUE DE MONTREAL
; TITLE OF INVENTION: PRO-PROTEIN CONVERTING ENZYME
; FILE REFERENCE: PRO-PROTEIN CONVERT ENZ
; CURRENT APPLICATION NUMBER: US/09/214,555B
; PRIOR FILING DATE: 1999-01-04
; PRIOR APPLICATION NUMBER: 60/021,008
; PRIOR FILING DATE: 1996-07-26
; PRIOR APPLICATION NUMBER: 2,203,745
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-555B-7

Query Match 9.1%; Score 82.5; DB 4; Length 915;

Best Local Similarity 26.0%; Pred. No. 1.8;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;

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Qy 72 RKEQKFDHLRDLCTSCASIC-----GQHPKOC-----AYFCEN 106
Db 774 --EDGRYFNG--QDCOPCHRFATCATGAGADGACINCTEGYFMD 813

RESULT 13
US-09-590-656-2

; Sequence 2, Application US/09590656
; Patent No. 6413932
; GENERAL INFORMATION:
; APPLICANT: Cerretti, Douglas P.
; APPLICANT: Borges, Luis G.
; APPLICANT: Fanslow, III, William C.
; TITLE OF INVENTION: TEK ANTAGONISTS
; FILE REFERENCE: 2900-A
; CURRENT APPLICATION NUMBER: US/09/590,656
; CURRENT FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: 60/137,889
; PRIOR FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 704
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-590-656-2

Query Match 8.9%; Score 81; DB 4; Length 704;

Best Local Similarity 24.2%; Pred. No. 1.8;
Matches 39; Conservative 15; Mismatches 63; Indels 44; Gaps 8;

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Db 262 RTCKERCSCG-----QEGCKSYVFCPLDPYGCSCATGKGLQCNBEACH-----FGFYGPDC 312

Qy 120 RORSGEVNNSDNGRYQGLEHRSSEASPALGLKLSADQV 160
Db 313 LRCSC---NNGEMCDRFQ-----GCLCSFGWQGLQCNBEACH 345

RESULT 14

US-09-590-656-1
; Sequence 1, Application US/09590656
; Patent No. 6413932
; GENERAL INFORMATION:
; APPLICANT: Cerretti, Douglas P.
; APPLICANT: Borges, Luis G.
; APPLICANT: Fanslow, III, William C.
; TITLE OF INVENTION: TEK ANTAGONISTS
; FILE REFERENCE: 2900-A
; CURRENT APPLICATION NUMBER: US/09/590,656
; CURRENT FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: 60/137,889
; PRIOR FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-590-656-1

Query Match 8.9%; Score 81; DB 4; Length 977;

Best Local Similarity 24.2%; Pred. No. 2.8;
Matches 39; Conservative 15; Mismatches 63; Indels 44; Gaps 8;

Qy 26 WTGVAMRSCPEEQYWDPLGTGCM-----SKTTCN-HQSQ 59
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Qy 120 RORSGEVNNSDNGRYQGLEHRSSEASPALGLKLSADQV 160
Db 313 LRCSC---NNGEMCDRFQ-----GCLCSFGWQGLQCNBEACH 345

RESULT 15
US-08-323-474-2

; Sequence 2, Application US/08323474
; Patent No. 5447860
; GENERAL INFORMATION:
; APPLICANT: Ziegler, Steven F.
; TITLE OF INVENTION: NOVEL TYROSINE KINASE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,474
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/905,600
; FILING DATE: 26-JUN-1992
; ATTORNEY/AGENT INFORMATION:

NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-323-474-2

Query Match 8.9%; Score 81; DB 1; Length 1124;
Best Local Similarity 24.2%; Pred. No. 3.3;
Matches 39; Conservative 15; Mismatches 63; Indels 44; Gaps 8;

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Qy 120 RQSGVEVNNSDNGRYQGLHRGSEASPALPGLKLSADQV 160
Db 313 LRCSG---NNGEMQDRFQ-----GCLCSFGWQGLQCEREGET 345

Search completed: February 4, 2003, 13:00:17
Job time: 17.4575 secs

GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: February 4, 2003, 12:59:16 ; Search time 10.753 Seconds
(without alignments)
342.239 Million cell updates/sec

Title: US-09-854-864-15
Perfect score: 909
Sequence: 1 MSGIGSRGRGRSRVDGEER.....SPALPGIKLSADQVALVYST 166

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Gapop 10.0 , Gapext 0.5

Searched: 129505 seqs, 22169297 residues

Total number of hits satisfying chosen parameters: 129505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications MA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	909	100.0	166	10 US-09-854-864-15	Sequence 15, Appl
2	909	100.0	293	9 US-09-779-050A-42	Sequence 42, Appl
3	909	100.0	293	9 US-10-084-971-2	Sequence 2, Appl
4	909	100.0	293	9 US-10-068-725-4	Sequence 4, Appl
5	909	100.0	293	9 US-09-302-863-2	Sequence 2, Appl
6	909	100.0	293	10 US-09-879-919-22	Sequence 12, Appl
7	909	100.0	293	10 US-09-854-864-14	Sequence 14, Appl
8	909	100.0	293	10 US-09-961-376-2	Sequence 18, Appl
9	904	99.4	291	9 US-09-854-864-18	Sequence 43, Appl
10	894.5	98.4	67	10 US-09-854-864-43	Sequence 16, Appl
11	393	43.2	59	10 US-09-854-864-16	Sequence 20, Appl
12	342	37.6	57	9 US-09-854-864-20	Sequence 47, Appl
13	279.5	30.7	38	9 US-09-779-050A-47	Sequence 46, Appl
14	224	24.6	37	9 US-09-779-050A-46	Sequence 45, Appl
15	218	24.0	32	9 US-09-779-050A-45	Sequence 44, Appl
16	168	18.5	81	10 US-09-779-050A-44	Sequence 13, Appl
17	93	10.2	463	9 US-09-854-864-13	Sequence 285, App
18	87.5	9.6	463	9 US-09-905-291A-285	Sequence 285, App
19	87.5	9.6	463	9 US-09-902-853-285	Sequence 285, App

20	87.5	9.6	463	9 US-09-907-824-285	Sequence 285, App
21	87.5	9.6	463	9 US-09-907-841-285	Sequence 285, App
22	87.5	9.6	463	9 US-09-904-011-285	Sequence 285, App
23	87.5	9.6	463	9 US-10-028-072-360	Sequence 360, App
24	87.5	9.6	463	9 US-09-906-742-285	Sequence 285, App
25	87.5	9.6	463	9 US-10-121-049-360	Sequence 360, App
26	87.5	9.6	463	9 US-10-123-904-360	Sequence 360, App
27	87.5	9.6	463	9 US-10-140-470-360	Sequence 360, App
28	87.5	9.6	463	10 US-09-909-320-285	Sequence 285, App
29	87.5	9.6	463	10 US-09-909-088B-285	Sequence 285, App
30	87	9.6	207	9 US-10-077-438-3	Sequence 3, Appl
31	87	9.6	292	10 US-10-077-137-3	Sequence 3, Appl
32	87	9.6	292	10 US-09-745-763-166	Sequence 166, App
33	86	9.5	231	10 US-09-840-795-19	Sequence 19, Appl
34	86	9.5	229	9 US-10-119-466-12	Sequence 12, Appl
35	84	9.2	77	10 US-09-840-795-17	Sequence 17, Appl
36	82.5	9.1	225	9 US-10-185-770-4	Sequence 4, Appl
37	81	8.9	586	9 US-10-092-390-4	Sequence 4, Appl
38	81	8.9	1140	9 US-10-092-390-2	Sequence 2, Appl
39	79.5	8.7	1172	9 US-09-974-298-56	Sequence 56, Appl
40	79.5	8.7	1172	10 US-09-919-172-16	Sequence 16, Appl
41	78.5	8.6	399	10 US-09-907-372-1	Sequence 1, Appl
42	77.5	8.5	220	10 US-10-042-141-54	Sequence 54, Appl
43	77.5	8.5	220	10 US-09-726-643-54	Sequence 54, Appl
44	77.5	8.5	514	10 US-09-800-729-124	Sequence 124, App
45	77.5	8.5	1745	10 US-09-800-729-89	Sequence 89, Appl

ALIGNMENTS

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RESULT 1
US-09-854-864-15
; Sequence 15, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THELL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLVS/ACP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-15

Query Match      100.0%; Score 909; DB 10; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.5e-75;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MSGIGSRGRGRSRVDGEERPPQGLMTGVAMRSCPEEQYMDPLLTGTCSCKTICNHQOR 60
DB      1 MSGIGSRGRGRSRVDGEERPPQGLMTGVAMRSCPEEQYMDPLLTGTCSCKTICNHQOR 60

QY      61 TCAACRSLCRKCKGKYDHLRDCSCAICGHPKQCAVFCENKLRSPVNLPELR 120
DB      61 TCAACRSLCRKCKGKYDHLRDCSCAICGHPKQCAVFCENKLRSPVNLPELR 120

QY      121 QRSGEVNNSDNGRGYQGLERHGESEAPALPGIKLSADQVALVYST 166
DB      121 QRSGEVNNSDNGRGYQGLERHGESEAPALPGIKLSADQVALVYST 166

RESULT 2
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US-09-779-050A-42
; Sequence 42, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-42

Query Match 100.0%; Score 909; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.8e-75;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 TCAAFCSRSLSCRKEQKGYDHLRDCISCAICGQHPKQCAVFCENKLRSPVNLPEELRR 120
Db 61 TCAAFCSRSLSCRKEQKGYDHLRDCISCAICGQHPKQCAVFCENKLRSPVNLPEELRR 120
Qy 121 QRSGEVNNSDNSGRYQGLGHERGSEASPALPGLKLSADQVALVYST 166
Db 121 QRSGEVNNSDNSGRYQGLGHERGSEASPALPGLKLSADQVALVYST 166

RESULT 3
US-10-084-971-2
; Sequence 2, Application US/10084971
; Publication No. US20020187526A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Neutrokin- α Binding Proteins and Methods Based Thereon
; FILE REFERENCE: PFS24PCT
; CURRENT APPLICATION NUMBER: US/10/084,971
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/533,822
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/126,599
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/188,208
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-084-971-2

Query Match 100.0%; Score 909; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.8e-75;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 TCAAFCSRSLSCRKEQKGYDHLRDCISCAICGQHPKQCAVFCENKLRSPVNLPEELRR 120

Qy 121 QRSGEVNNSDNSGRYQGLGHERGSEASPALPGLKLSADQVALVYST 166
Db 121 QRSGEVNNSDNSGRYQGLGHERGSEASPALPGLKLSADQVALVYST 166

RESULT 4
US-10-068-725-4
; Sequence 4, Application US/10068725
; Publication No. US20030012783A1
; GENERAL INFORMATION:
; APPLICANT: Kindvogel, Wayne
; TITLE OF INVENTION: Antibodies That Bind Both BCMA and TACI
; FILE REFERENCE: 01-04
; CURRENT APPLICATION NUMBER: US/10/068,725
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/270,274
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/283,447
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-725-4

Query Match 100.0%; Score 909; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.8e-75;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 TCAAFCSRSLSCRKEQKGYDHLRDCISCAICGQHPKQCAVFCENKLRSPVNLPEELRR 120
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Db 121 QRSGEVNNSDNSGRYQGLGHERGSEASPALPGLKLSADQVALVYST 166

RESULT 5
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; Sequence 2, Application US/09302863
; Publication No. US20030022233A1
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G
; APPLICANT: Din, Manwan S.
; TITLE OF INVENTION: METHODS OF USE OF THE TACI/TACI-L INTERACTION
; FILE REFERENCE: 2519
; CURRENT APPLICATION NUMBER: US/09/302,863
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Human
US-09-302-863-2

Query Match 100.0%; Score 909; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.8e-75;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166
Db 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166

RESULT 6

US-09-879-919-22
; Sequence 22, Application US/09879919
; Patent No. US20020064829A1
; GENERAL INFORMATION:

; APPLICANT: Yu, Guo-Liang, et al.

; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: P2533P1

; CURRENT APPLICATION NUMBER: US/09/879,919

; PRIOR FILING DATE: 2001-06-14

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/277,978

; PRIOR FILING DATE: 2001-03-23

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/254,875

; PRIOR FILING DATE: 2000-12-13

; PRIOR APPLICATION NUMBER: 60/241,952

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/211,537

; PRIOR FILING DATE: 2000-06-15

; PRIOR APPLICATION NUMBER: 08/815,783

; PRIOR FILING DATE: 1997-03-12

; PRIOR APPLICATION NUMBER: 60/016,812

; PRIOR FILING DATE: 1996-03-14

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 22

; LENGTH: 293

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-879-919-22

Query Match
Best Local Similarity 100.0%; Score 909; DB 10; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.8e-75;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRRGGRSVYDOERFPQGLMTGVAMRSCPEBOYMDPLGTGMSCKTICNHQSOR 60
Db 1 MSGLSRRGGRSVYDOERFPQGLMTGVAMRSCPEBOYMDPLGTGMSCKTICNHQSOR 60
QY 61 TCAACRSLSCRKEQGYDHLRDCISCAICGHPKQCAVFCENKLRSPVNLPEELR 120
Db 61 TCAACRSLSCRKEQGYDHLRDCISCAICGHPKQCAVFCENKLRSPVNLPEELR 120

QY 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166
Db 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166

RESULT 7

US-09-854-864-14
; Sequence 14, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:

; APPLICANT: YU, GANG
; APPLICANT: THEIL, LARS EYDE

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-684B

; CURRENT APPLICATION NUMBER: US/09/854,864

; PRIOR FILING DATE: 2001-09-11

; PRIOR APPLICATION NUMBER: US 60/204,039

; PRIOR FILING DATE: 2000-05-12

; PRIOR APPLICATION NUMBER: US 60/214,591

; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-14

Query Match
Best Local Similarity 100.0%; Score 909; DB 10; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.8e-75;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRRGGRSVYDOERFPQGLMTGVAMRSCPEBOYMDPLGTGMSCKTICNHQSOR 60
Db 1 MSGLSRRGGRSVYDOERFPQGLMTGVAMRSCPEBOYMDPLGTGMSCKTICNHQSOR 60
QY 61 TCAACRSLSCRKEQGYDHLRDCISCAICGHPKQCAVFCENKLRSPVNLPEELR 120
Db 61 TCAACRSLSCRKEQGYDHLRDCISCAICGHPKQCAVFCENKLRSPVNLPEELR 120
QY 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166
Db 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166

RESULT 8

US-09-961-376-2
; Sequence 2, Application US/09961376
; Patent No. US20020106736A1
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR17

; FILE REFERENCE: P2524P1

; CURRENT APPLICATION NUMBER: US/09/961,376

; PRIOR FILING DATE: 2001-09-25

; PRIOR APPLICATION NUMBER: 60/254,874

; PRIOR FILING DATE: 2000-12-13

; PRIOR APPLICATION NUMBER: 60/235,991

; PRIOR FILING DATE: 2000-09-26

; PRIOR APPLICATION NUMBER: 09/533,822

; PRIOR FILING DATE: 2000-03-24

; PRIOR APPLICATION NUMBER: 60/188,208

; PRIOR FILING DATE: 2000-03-10

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 293

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-961-376-2

Query Match
Best Local Similarity 100.0%; Score 909; DB 10; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.8e-75;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGLSRRGGRSVYDOERFPQGLMTGVAMRSCPEBOYMDPLGTGMSCKTICNHQSOR 60
Db 1 MSGLSRRGGRSVYDOERFPQGLMTGVAMRSCPEBOYMDPLGTGMSCKTICNHQSOR 60
QY 61 TCAACRSLSCRKEQGYDHLRDCISCAICGHPKQCAVFCENKLRSPVNLPEELR 120
Db 61 TCAACRSLSCRKEQGYDHLRDCISCAICGHPKQCAVFCENKLRSPVNLPEELR 120
QY 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166
Db 121 ORSGEVNNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166

RESULT 9

US-09-854-864-18
; Sequence 18, Application US/09854864
; Patent No. US20020081296A1

```
/ GENERAL INFORMATION:
/ APPLICANT: THEHILL, LARS EYDE
/ APPLICANT: YU, GANG
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
/ FILE REFERENCE: A-686B
/ CURRENT APPLICATION NUMBER: US/09/854,864
/ CURRENT FILING DATE: 2001-09-11
/ PRIOR APPLICATION NUMBER: US 60/204,039
/ PRIOR FILING DATE: 2000-05-12
/ PRIOR APPLICATION NUMBER: US 60/214,591
/ PRIOR FILING DATE: 2000-06-27
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 18
/ LENGTH: 397
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-854-864-18
```

```
Query Match          99.4%; Score 904; DB 10; Length 397;
Best Local Similarity 100.0%; Pred. No. 1,1e-74;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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Qy 1 MSGLGRSRGRSRVDQERFPQGLMTGVAMRSCPEEQYWDPLGTGCMCKTICNHOSOR 60
Db 1 MSGLGRSRGRSRVDQERFPQGLMTGVAMRSCPEEQYWDPLGTGCMCKTICNHOSOR 60
Qy 61 TCAAFCRSLSCREKQKFDHLRDCISCAICGHPKQCAVFCENKLSPVNLPPELRR 120
Db 61 TCAAFCRSLSCREKQKFDHLRDCISCAICGHPKQCAVFCENKLSPVNLPPELRR 120
Qy 121 ORSGVEYNNSDNSGRYQGLEHRSSEASPALPGIKLSADQVALVYS 165
Db 121 ORSGVEYNNSDNSGRYQGLEHRSSEASPALPGIKLSADQVALVYS 165
```

```
RESULT 10
US-09-779-050A-43
/ Sequence 43, Application US/09779050A
/ Patent No. US20020160416A1
/ GENERAL INFORMATION:
/ APPLICANT: BOYLE, WILLIAM
/ APPLICANT: HSU, HAILING
/ TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
/ FILE REFERENCE: A-570B
/ CURRENT APPLICATION NUMBER: US/09/779,050A
/ CURRENT FILING DATE: 2001-02-12
/ PRIOR APPLICATION NUMBER: 60/181,800
/ PRIOR FILING DATE: 2000-02-11
/ NUMBER OF SEQ ID NOS: 52
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 43
/ LENGTH: 291
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-779-050A-43
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Query Match          98.4%; Score 894.5; DB 9; Length 291;
Best Local Similarity 99.4%; Pred. No. 5,7e-74;
Matches 165; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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Qy 1 MSGLGRSRGRSRVDQERFPQGLMTGVAMRSCPEEQYWDPLGTGCMCKTICNHOSOR 60
Db 1 MSGLGRSRGRSRVDQERFPQGLMTGVAMRSCPEEQYWDPLGTGCMCKTICNHOSOR 60
Qy 61 TCAAFCRSLSCREKQKFDHLRDCISCAICGHPKQCAVFCENKLSPVNLPPELRR 120
Db 61 TCAAFCRSLSCREKQKFDHLRDCISCAICGHPKQCAVFCENKLSPVNLPPELRR 120
Qy 121 ORSGVEYNNSDNSGRYQGLEHRSSEASPALPGIKLSADQVALVYS 166
Db 121 ORSGVEYNNSDNSGRYQGLEHRSSEASPALPGIKLSADQVA-VYST 165
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```
RESULT 11
US-09-854-864-16
/ Sequence 16, Application US/09854864
/ Patent No. US20020081296A1
/ GENERAL INFORMATION:
/ APPLICANT: THEHILL, LARS EYDE
/ APPLICANT: YU, GANG
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
/ FILE REFERENCE: A-686B
/ CURRENT APPLICATION NUMBER: US/09/854,864
/ CURRENT FILING DATE: 2001-09-11
/ PRIOR APPLICATION NUMBER: US 60/204,039
/ PRIOR FILING DATE: 2000-05-12
/ PRIOR APPLICATION NUMBER: US 60/214,591
/ PRIOR FILING DATE: 2000-06-27
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 16
/ LENGTH: 67
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-854-864-16
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Query Match          43.2%; Score 393; DB 10; Length 67;
Best Local Similarity 94.4%; Pred. No. 3e-29;
Matches 67; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
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```
Qy 34 CPEEQYWDPLGTGCMCKTICNHOSQRTCAAFCRSLSCREKQKFDHLRDCISCAIC 93
Db 1 CPEEQYWDPLGTGCMCKTICNHOSQRTCAAF-----CRKQKQKFDHLRDCISCAIC 56
Qy 94 GQHPKQCAVFC 104
Db 57 GQHPKQCAVFC 67
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```
RESULT 12
US-09-854-864-20
/ Sequence 20, Application US/09854864
/ Patent No. US20020081296A1
/ GENERAL INFORMATION:
/ APPLICANT: THEHILL, LARS EYDE
/ APPLICANT: YU, GANG
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
/ FILE REFERENCE: A-686B
/ CURRENT APPLICATION NUMBER: US/09/854,864
/ CURRENT FILING DATE: 2001-09-11
/ PRIOR APPLICATION NUMBER: US 60/204,039
/ PRIOR FILING DATE: 2000-05-12
/ PRIOR APPLICATION NUMBER: US 60/214,591
/ PRIOR FILING DATE: 2000-06-27
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 20
/ LENGTH: 59
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-854-864-20
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Query Match          37.6%; Score 342; DB 10; Length 59;
Best Local Similarity 100.0%; Pred. No. 1,1e-24;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 34 CPEEQYWDPLGTGCMCKTICNHOSQRTCAAFCRSLSCREKQKFDHLRDCISCAIC 92
Db 1 CPEEQYWDPLGTGCMCKTICNHOSQRTCAAFCRSLSCREKQKFDHLRDCISCAIC 59
```

RESULT 13

US-09-779-050A-47
; Sequence 47, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-47

Query Match
Best Local Similarity 30.7%; Score 279.5; DB 9; Length 57;
98.3%; Pred. No. 4.8e-19;
Matches 57; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 108 LRSFVNLPELRRDRSGEYVNNDSNGRYQGLEHRSSEASPALPGIKLSADQVALYVS 165
Db 1 LRSFVNLPELRRDRSGEYVNNDSNGRYQGLEHRSSEASPALPGIKLSADQVA-VYS 57

RESULT 14
US-09-779-050A-46
; Sequence 46, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-46

Query Match
Best Local Similarity 24.6%; Score 224; DB 9; Length 38;
100.0%; Pred. No. 3.3e-14;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 SCRKEQGFYDHLIRDCISCAISICGHPKQCAVFCENK 107
Db 1 SCRKEQGFYDHLIRDCISCAISICGHPKQCAVFCENK 38

RESULT 15
US-09-779-050A-45
; Sequence 45, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-45

Query Match
Best Local Similarity 24.0%; Score 218; DB 9; Length 37;
100.0%; Pred. No. 1.1e-13;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 SCPEQYWDPLIGTCMCKTICNHSQRTCAAFCSL 69
Db 1 SCPEQYWDPLIGTCMCKTICNHSQRTCAAFCSL 37

Search completed: February 4, 2003, 13:05:58
Job time : 11.753 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2003, 12:52:56 / Search time 42.3401 Seconds
(without alignments) -
522.427 Million cell updates/sec

Title: US-09-854-864-15

Perfect score: 1 MSGIGRSRGRSGRVDQBER.....SPALPGKLSADQVALVYST 166

Sequence: BLOSUM62

Scoring table: Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	909	100.0	166	19	AAW75785
2	909	100.0	166	23	AAE15494
3	909	100.0	265	22	AAE09244
4	909	100.0	293	19	AAW75783
5	909	100.0	293	21	AAE15494
6	909	100.0	293	21	AAE09240
7	909	100.0	293	22	AAE09240
8	909	100.0	293	22	AAE09240
9	909	100.0	293	23	AAU95512
10	909	100.0	293	23	AAE15488

11	909	100.0	293	23	AAO14130
12	909	100.0	293	23	AAU75408
13	909	100.0	293	23	AAE15493
14	909	100.0	293	23	AAU09900
15	909	100.0	293	23	AAO14135
16	904	99.4	397	23	AAE15498
17	894.5	98.4	291	23	AAU10949
18	881	96.9	404	23	AAO14136
19	651	71.6	366	23	AAO14132
20	599	65.9	247	21	AAE15498
21	480.5	54.0	334	23	AAO14133
22	419.5	46.1	249	21	AAE15498
23	342	37.6	59	23	AAE15500
24	279.5	30.7	57	23	AAU10953
25	224	24.6	38	23	AAU10952
26	218	24.0	37	23	AAU10951
27	204	22.4	34	23	AAE15496
28	201	22.1	33	23	AAE15495
29	168	18.5	32	23	AAU10950
30	95	10.5	32	23	AAE15491
31	93	10.2	1589	22	AAE15491
32	93	10.2	1727	22	AAE15491
33	93	10.2	1878	22	AAE15491
34	92	10.1	266	22	AAE15491
35	89	9.8	1878	19	AAE15491
36	88.5	9.7	665	22	AAE15491
37	88	9.7	795	22	AAE15491
38	87.5	9.6	463	20	AAE15491
39	87.5	9.6	463	21	AAE15491
40	87.5	9.6	463	21	AAE15491
41	87.5	9.6	463	22	AAE15491
42	87.5	9.6	463	22	AAE15491
43	87.5	9.6	463	22	AAE15491
44	87.5	9.6	463	22	AAE15491
45	87	9.6	251	22	AAE15491

ALIGNMENTS

RESULT 1	AAW75785	standard; Protein; 166 AA.
XX	AAW75785	
AC	AAW75785	
XX	18-JAN-1999	(first entry)
DT	18-JAN-1999	
XX		
XX		
DE	Human lymphocyte surface receptor extracellular domain.	
XX		
XX		
KW	TAC1; transmembrane activator and CAML-interactor;	
KW	calcium signal-modulating cyclophilin ligand; human;	
KW	lymphocyte surface receptor; human; B-cell; B lymphocyte;	
KW	infection; cancer; rheumatoid arthritis; autoimmune disease;	
KW	glomerulonephritis; immunosuppressive; graft versus host disease;	
KW	transplant rejection; therapy; signal transduction.	
XX		
OS	Homo sapiens.	
XX		
PN	WO9839361-A1.	
XX		
PD	11-SEP-1998.	
XX		
PF	03-MAR-1998;	98WO-US04270.
XX		
PR	03-MAR-1997;	97US-0810572.
XX		
PA	(STUD-) ST JUDE CHILDREN'S RES HOSPITAL.	
XX		
PI	Bram RJ, Von Bulow G;	
XX		
DR	WPI; 1998-506346/43.	
DR	N-PSDB; AAV57330.	

Human transmembran
Tumor necrosis fa
Human transmembran
Human AGP-3 relat
Protein of N-termi
Human TAC1-immunog
Human AGP-3 recept
Protein of a compl
Protein of hTAC1 (i
Human BR43x2, an i
Protein of hTAC1 (i
A murine znfx, a
Human TAC1 cytein
Human AGP-3 recept
Human AGP-3 recept
Human AGP-3 recept
Human TAC1 cytein
Human TAC1 cytein
Human AGP-3 recept
Human TANGO 140-2.
Human polypeptide
Human protein sequ
Human polypeptide
Human polypeptide
Human BAZ2-alpha p
Drosophila melanog
Novel human diagno
Amino acid sequenc
Neuron-associated
Human PRO328 antit
Human membrane or
Human PRO328 prote
Human angiotensin
Human mature stem

XX New isolated transmembrane activator protein - used to develop
PT products for treating e.g. infections, cancers, autoimmune and
PT inflammatory conditions, transplant rejection or graft-versus-host
PT disease
XX
XX Claim 8, Page 73, 89pp; English.
XX
XX This is the amino acid sequence of the N-terminal, i.e. the
CC extracellular, domain of novel human transmembrane activator and
CC CAMI-interactor (TACI) protein (see AA075783). TACI is a lymphocyte
CC receptor protein that is involved in the calcium activation pathway.
CC It is normally present in B-lymphocytes, and to a much lesser extent
CC in immature T-lymphocytes, and can therefore be targeted to
CC specifically regulate B cell responses without affecting T cell
CC activity. The extracellular domain of TACI functions as a binding
CC site for a ligand that stimulates the activation of the cell by
CC inducing the binding of the C-terminal portion (see AA075784) of
CC TACI to the N-terminal domain of CAMI. A recombinant form of the
CC extracellular portion of TACI acts as a dominant-negative or
CC blocking agent and acts to suppress the immune system. It can be
CC used to treat or prevent autoimmune disease, graft rejection or
CC graft versus host disease. The extracellular region is also used
CC in a claimed method for identifying a ligand for TACI, in which
CC binding of a candidate molecule is determined by detecting cellular
CC activation of the AP-1, CAMP or NF-KB pathway, of NF-AT
CC transcription factor, or of NF-AT dependent transcription.
CC
XX Sequence 166 AA:
SQ
Query Match 100.0%; Score 909; DB 19; Length 166;
Best Local Similarity 100.0%; Pred. No. 2.8e-83;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSGLSRRGSRGRVQDERFPQGLMTGVAMRSCPEQYMDPLGTGCMCKTICNHQSOR 60
DB 1 MSGLSRRGSRGRVQDERFPQGLMTGVAMRSCPEQYMDPLGTGCMCKTICNHQSOR 60
QY 61 TCAAFCRSLSCRKEQGFYDHLNRDLCISGQHPKQCAVFCENKLRSPVNLPELRR 120
DB 61 TCAAFCRSLSCRKEQGFYDHLNRDLCISGQHPKQCAVFCENKLRSPVNLPELRR 120
QY 121 QRSGEVNNSDNSGRYQGLEHRSSEASPALPGIKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRYQGLEHRSSEASPALPGIKLSADQVALVYST 166
RESULT 2
AAE15494
ID AAE15494 standard; Protein; 166 AA.
AC AAE15494;
XX
XX 12-MAR-2002 (first entry)
XX
XX Human TACI extracellular domain.
XX
XX Human: transmembrane activator and intracellular CAMI interactor; TACI;
KW cytoactive; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastroenteric; pancreatic;
KW prostate; inflammatory; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis.
XX
XX Homo sapiens.
OS
XX WO200187979-A2.
XX
XX 22-NOV-2001.
XX
XX 14-MAY-2001; 2001WO-US15567.
PF

XX
PR 12-MAY-2000; 2000US-204039P.
PR 27-JUN-2000; 2000US-214591P.
PR 14-MAY-2001; 2001US-0214591.
XX
XX (AMGE-) AMGEN INC.
XX
XX The111 LE, Yu G;
XX
XX WPI, 2002-066686/09.
XX
XX Claim 1, Fig 12A, 94pp; English.
XX
XX The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAMI interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering
CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC family ligand), having the consensus sequence, but not the extracellular region
CC of BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human TACI protein extracellular domain.
XX
XX Sequence 166 AA:
SQ
Query Match 100.0%; Score 909; DB 23; Length 166;
Best Local Similarity 100.0%; Pred. No. 2.8e-83;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSGLSRRGSRGRVQDERFPQGLMTGVAMRSCPEQYMDPLGTGCMCKTICNHQSOR 60
DB 1 MSGLSRRGSRGRVQDERFPQGLMTGVAMRSCPEQYMDPLGTGCMCKTICNHQSOR 60
QY 61 TCAAFCRSLSCRKEQGFYDHLNRDLCISGQHPKQCAVFCENKLRSPVNLPELRR 120
DB 61 TCAAFCRSLSCRKEQGFYDHLNRDLCISGQHPKQCAVFCENKLRSPVNLPELRR 120
QY 121 QRSGEVNNSDNSGRYQGLEHRSSEASPALPGIKLSADQVALVYST 166
DB 121 QRSGEVNNSDNSGRYQGLEHRSSEASPALPGIKLSADQVALVYST 166
RESULT 3
AAE09244
ID AAE09244 standard; Protein; 265 AA.
AC AAE09244;
XX
XX 19-NOV-2001 (first entry)
XX
XX Human TACI splice variant protein.
XX
XX Human: TNF, tumour necrosis factor; TACI-1; APRIL; TNF receptor;
KW TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
KW psoriasis.
XX
XX Homo sapiens.
OS

XX WO200160397-A1.
 XX 23-AUG-2001.
 XX 28-NOV-2000; 2000WD-US32378.
 XX 16-FEB-2000; 2000US-0182938.
 XX 22-AUG-2000; 2000US-0226986.
 PA (GETH) GENENTECH INC.
 PI Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Maresters SA, Picetti RM,
 PI Yan M;
 XX WPI; 2001-541628/60.
 XX
 PT Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
 PT activity, for treating autoimmune disorders and cancer, comprises
 PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
 PT antagonists -
 XX
 PS Example 1; Fig 6; 160pp; English.
 XX
 CC The invention relates to methods of using one or more agonists or
 CC antagonists to modulate the activity of the members of TNF (tumour
 CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR)
 CC e.g. TACI or BCMA. The method is useful for treating pathological
 CC conditions or diseases associated with increased TALL-1 and APRIL
 CC expression or activity. TALL-1 and APRIL antagonists are used to
 CC block the interaction between APRIL and TALL-1 with TACI or BCMA.
 CC They are useful for treating a mammal suffering from cancer such
 CC as leukaemia, lymphoma, myeloma, cancers of lung and colon and
 CC autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,
 CC psoriasis and lupus erythematosus. The present sequence is human
 CC TACI splice variant protein.
 XX
 SQ Sequence 265 AA;
 Query Match 100.0%; Score 909; DB 22; Length 265;
 Best Local Similarity 100.0%; Pred. No. 4,9e-83;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSGIGRSRRGRSRVDQERFPQGLMTGVAMRSCPEEYWDPLLTGTCMSCKTICNHQSOR 60
 Db 1 MSGIGRSRRGRSRVDQERFPQGLMTGVAMRSCPEEYWDPLLTGTCMSCKTICNHQSOR 60
 QY 61 TCAAFCRSLSCRKQKGYDHLRDCISCASICGQHPKQCAVFCENKLRSPVNLPEELRR 120
 Db 61 TCAAFCRSLSCRKQKGYDHLRDCISCASICGQHPKQCAVFCENKLRSPVNLPEELRR 120
 QY 121 QRSGEVENNSDNGRKYQGLEHGRSEASPALPELKLISADQVNLVYST 166
 Db 121 QRSGEVENNSDNGRKYQGLEHGRSEASPALPELKLISADQVNLVYST 166
 RESULT 4
 ID AAW75783 standard; Protein: 293 AA.
 XX AAW75783;
 AC AAW75783;
 XX 18-JAN-1999 (first entry)
 DT 18-JAN-1999 (first entry)
 XX Human lymphocyte surface receptor TACI.
 DE Human lymphocyte surface receptor TACI.
 XX TACI; transmembrane activator and CAML-interactor;
 KW calcium signal-modulating cyclophilin ligand; human;
 KW lymphocyte surface receptor; human; B-cell; B lymphocyte;
 KW infection; cancer; rheumatoid arthritis; autoimmune disease;
 KW glomerulonephritis; immunosuppressive; graft versus host disease;
 KW transplant rejection; therapy.
 KM

OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..166
 FT /label= Extracellular_domain
 FT /note= "Claim 8"
 FT Domain 167..186
 FT /label= Transmembrane_domain
 FT Domain 187..294
 FT /label= Cytoplasmic_domain
 FT /note= "Claim 6"
 FT Peptide 34..71
 FT /note= "TNFR_NGFR motif"
 FT
 XX WO9839361-A1.
 XX 11-SEP-1998.
 XX 03-MAR-1998; 98WO-US04270.
 XX 03-MAR-1997; 97US-0810572.
 XX (STUD-) ST JUDE CHILDREN'S RES HOSPITAL.
 PA Bram RJ, Von Bulow G;
 PI WPI; 1998-506346/43.
 DR N-PSDB; AAV57328.
 XX
 PT New isolated transmembrane activator protein - used to develop
 PT products for treating e.g. infections, cancers, autoimmune and
 PT inflammatory conditions, transplant rejection or graft-versus-host
 PT disease
 XX
 PS Claim 20; Fig 2a; 89pp; English.
 XX
 CC This is the amino acid sequence of novel human transmembrane
 CC activator and CAML-interactor (TACI) protein, a lymphocyte receptor
 CC protein that is involved in the calcium activation pathway. TACI
 CC is normally present in B-lymphocytes, and to a much lesser extent
 CC in immature T-lymphocytes, and can therefore be targeted to
 CC specifically regulate B cell responses without affecting T cell
 CC activity. TACI cDNA (seeV57328) was isolated from a B-lymphocyte
 CC cDNA library using a yeast two-hybrid assay. Also claimed are
 CC the C-terminal (see AAW75784) and N-terminal (see AAW75785) fragments
 CC of TACI, recombinant DNA constructs, unicellular hosts, and
 CC antibodies to TACI protein. Methods are claimed for identifying a
 CC ligand for TACI and for identifying immunosuppressive drugs that
 CC selectively block the action of B lymphocytes without affecting
 CC mature T lymphocytes. TACI can be activated to increase immune
 CC system activity, e.g. for treating infections or cancers. It can
 CC be blocked to provide immunosuppression, e.g. for treating
 CC autoimmune and inflammatory conditions such as immune complex-
 CC induced vasculitis, glomerulonephritis, haemolytic anaemia,
 CC myasthenia gravis, type II collagen-induced arthritis, experimental
 CC allergic and hyperacute xenograft rejection, rheumatoid arthritis,
 CC systemic lupus erythematosus, transplant rejection, cancer or
 CC graft versus host disease.
 XX
 SQ Sequence 293 AA;
 Query Match 100.0%; Score 909; DB 19; Length 293;
 Best Local Similarity 100.0%; Pred. No. 5,6e-83;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSGIGRSRRGRSRVDQERFPQGLMTGVAMRSCPEEYWDPLLTGTCMSCKTICNHQSOR 60
 Db 1 MSGIGRSRRGRSRVDQERFPQGLMTGVAMRSCPEEYWDPLLTGTCMSCKTICNHQSOR 60
 QY 61 TCAAFCRSLSCRKQKGYDHLRDCISCASICGQHPKQCAVFCENKLRSPVNLPEELRR 120
 Db 61 TCAAFCRSLSCRKQKGYDHLRDCISCASICGQHPKQCAVFCENKLRSPVNLPEELRR 120

```
Qy 121 QRSGEVNNNSDNGRYQGLEHRSSEASPALPGIKLSADQVALVYST 166
Db 121 QRSGEVNNNSDNGRYQGLEHRSSEASPALPGIKLSADQVALVYST 166

RESULT 5
ID AAB36312 standard; Protein; 293 AA.
AC AAB36312;
XX
XX
XX 26-FEB-2001 (first entry)
XX
XX
XX Human neutrokin-alpha binding protein TR17 SEQ ID NO:2.
XX
XX
XX Human; neutrokin-alpha binding protein; NAR protein; TR17; cytostatic;
XX immunosuppressive; neutrotropic; neuroprotective; antiviral; antiallergic;
XX hepatotropic; antidiabetic; antiinflammatory; antitumor; cardiac;
XX ophthalmological; gene therapy; immunodeficiency disorder; diagnosis;
XX autoimmune disorder.
XX
XX Homo sapiens.
XX
XX WO200058362-A1.
XX
XX 05-OCT-2000.
XX
XX 24-MAR-2000; 2000WO-US07966.
XX
XX 26-MAR-1999; 99US-0126599.
XX 10-MAR-2000; 2000US-0188208.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Ullrich S, Baker K;
XX
XX WPI; 2000-602359/57.
XX
XX N-PSDB; AAC64602.
XX
XX Nucleic acid encoding a neutrokin-alpha receptor (NAR) such as TR17,
XX useful for producing TR17 protein which is used in the treatment and
XX diagnosis of autoimmune and immunodeficiency disorders -
XX
XX Claim 1; Fig 1; 398pp; English.
XX
XX The present sequence represents the human neutrokin-alpha binding (NAR)
XX protein designated TR17. TR17 has cytostatic, immunosuppressive,
XX neurotropic, neuroprotective, antiviral, antiallergic, hepatotropic,
XX antidiabetic, antiinflammatory, antitumor, cardiac and ophthalmological
XX activities and can be used in gene therapy. The TR17 protein and
XX antibodies are useful for treating and diagnosing immunodeficiency
XX disorders and autoimmune disorders. The TR17 polypeptides,
XX polynucleotides, antibodies, agonists and/or antagonists are used for
XX treating various other diseases defined in the specification and as
XX research tools for studying the phenotypic effects that result from
XX inhibiting TR17/TR17 ligand interactions on various cell types.
XX
XX Sequence 293 AA:
XX
XX Query Match 100.0%; Score 909; DB 21; Length 293;
XX Best Local Similarity 100.0%; Pred. No. 5.6e-83;
XX Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
```

```
Db 121 QRSGEVNNNSDNGRYQGLEHRSSEASPALPGIKLSADQVALVYST 166
Db 121 QRSGEVNNNSDNGRYQGLEHRSSEASPALPGIKLSADQVALVYST 166

RESULT 6
ID AAY94000 standard; Protein; 293 AA.
AC AAY94000;
XX
XX
XX 20-OCT-2000 (first entry)
XX
XX
XX A transmembrane activator and CAML-interactor (TACI).
XX
XX
XX Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
XX transmembrane activator and CAML-interactor; tumor necrosis factor; TNF;
XX ztnf4 activity; antibody production; autoimmune disease; amyloidosis;
XX systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
XX rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
XX end stage renal failure; glomerulonephritis; vasculitis; nephritis;
XX renal neoplasia; multiple myeloma; lymphoma; light chain neuropathy;
XX immune response; immunosuppression; graft rejection; joint pain;
XX graft versus host disease; inflammation; swelling; anaemia; septic shock;
XX insulin dependent diabetes mellitus; Crohn's disease; hypertension;
XX renal artery stenosis; occlusion; cholesterol; renal emboli.
XX
XX
XX Homo sapiens.
XX
XX WO200040716-A2.
XX
XX 13-JUL-2000.
XX
XX 07-JAN-2000; 2000WO-US00396.
XX
XX 07-JAN-1999; 99US-0226533.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Gross JA, Xu W, Madden K, Yee DP;
XX
XX WPI; 2000-452538/39.
XX
XX N-PSDB; AAA58558.
XX
XX Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,
XX renal disease, graft versus host disease, and inflammation, comprises
XX administering a BR43x2, TACI or BCMA extracellular domain polypeptide -
XX
XX Disclosure; Page 149-150; 175pp; English.
XX
XX The present sequence represents a human transmembrane activator and
XX CAML-interactor (TACI) receptor. TACI is a tumour necrosis factor (TNF)
XX receptor. The extracellular domains of BR43x2 (an isoform of TACI), TACI
XX or BCMA (a related B cell protein) receptor contain a cysteine rich
XX domain, and are used for inhibiting ztnf4 activity. Ztnf4 is a TNF
XX ligand. They may also be used for inhibiting BR43x2, TACI or BCMA
XX receptor-ligand engagement associated with activated or resting B
XX lymphocytes, effector T-cells, or with antibody production. The
XX antibody production is associated with an autoimmune disease selected
XX from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis
XX and rheumatoid arthritis. The ztnf4 activity and BR43x2, TACI or BCMA
XX receptor-ligand engagement is associated with asthma, bronchitis,
XX emphysema, end stage renal failure, glomerulonephritis, vasculitis,
XX nephritis, pyelonephritis, renal neoplasia, multiple myelomas, lymphomas,
XX light chain neuropathy, amyloidosis, moderating immune response,
XX immunosuppression, graft rejection, graft versus host disease,
XX inflammation, insulin dependent diabetes mellitus, Crohn's disease, joint
XX pain, swelling, anaemia, or septic shock. BR43x2, TACI, and BCMA
XX polypeptides, fusions, antibodies, agonists or antagonists can be used
XX to treat hypertension, renal artery stenosis, or occlusion, and
XX cholesterol or renal emboli.
XX
XX Sequence 293 AA:
XX
XX Query Match 100.0%; Score 909; DB 21; Length 293;
```

Best Local Similarity	100.0%;	Pred. No. 5.6e-83;	Matches 166;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MSGGRSHRGRSRVDOEERFPQGLMTGVAMRSCEPEQYMDPLGTGMSCKTICNHQSQR	60				
Db	1	MSGGRSHRGRSRVDOEERFPQGLMTGVAMRSCEPEQYMDPLGTGMSCKTICNHQSQR	60				
Qy	61	TCAAFCSRSLSCRKQKGFYDHLRDCISCAISCGQHPKQCAVFCENKLRSPVNLPEELRR	120				
Db	61	TCAAFCSRSLSCRKQKGFYDHLRDCISCAISCGQHPKQCAVFCENKLRSPVNLPEELRR	120				
Qy	121	QRSGEVNNSDNGRYOGLERHGSASPALPGLKLSADQVALVYST	166				
Db	121	QRSGEVNNSDNGRYOGLERHGSASPALPGLKLSADQVALVYST	166				
RESULT 7							
AAE09240	ID	AAE09240 standard;	Protein; 293 AA.				
XX	AC	AAE09240;					
XX	DE	19-NOV-2001 (first entry)					
XX	DE	Human TACI protein.					
XX	KW	Human; TNF; tumour	necrosis factor; TALL-1; APRIL; TNF receptor;				
XX	KW	TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;					
XX	KW	autoimmune disease; rheumatoid arthritis; multiple sclerosis;					
XX	KW	psoriasis.					
XX	OS	Homo sapiens.					
XX	PN	WO200160397-A1.					
XX	PD	23-AUG-2001.					
XX	PP	28-NOV-2000; 2000WO-US32378.					
XX	PR	16-FEB-2000; 2000US-0182938.					
XX	PR	22-AUG-2000; 2000US-0226986.					
XX	PA	(GETH) GENENTECH INC.					
XX	PI	Ashtkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pictri RM;					
XX	PI	Yan M;					
XX	DR	WPI; 2001-541628/60.					
XX	DR	N-PSDB; AAD15901.					
XX	PT	Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological					
XX	PT	activity for treating autoimmune disorders and cancer, comprises					
XX	PT	antagonists -					
XX	PS	Example 1; Fig 1; 160pp; English.					
XX	CC	The invention relates to methods of using one or more agonists or					
XX	CC	antagonists to modulate the activity of the members of TNF (tumour					
XX	CC	necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR)					
XX	CC	e.g. TACI or BCMA. The method is useful for treating pathological					
XX	CC	conditions or diseases associated with increased TALL-1 and APRIL					
XX	CC	expression or activity. TALL-1 and APRIL antagonists are used to					
XX	CC	block the interaction between APRIL and TALL-1 with TACI or BCMA.					
XX	CC	They are useful for treating a mammal suffering from cancer such					
XX	CC	as leukaemia, lymphoma, cancers of lung and colon and					
XX	CC	autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,					
XX	CC	psoriasis and lupus erythematosus. The present sequence is human					
XX	CC	TACI protein.					
XX	CC	Sequence 293 AA;					
XX	CC	Query Match	100.0%; Score 909; DB 22; Length 293;				

Best Local Similarity	100.0%;	Pred. No. 5.6e-83;	Matches 166;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MSGGRSHRGRSRVDOEERFPQGLMTGVAMRSCEPEQYMDPLGTGMSCKTICNHQSQR	60				
Db	1	MSGGRSHRGRSRVDOEERFPQGLMTGVAMRSCEPEQYMDPLGTGMSCKTICNHQSQR	60				
Qy	61	TCAAFCSRSLSCRKQKGFYDHLRDCISCAISCGQHPKQCAVFCENKLRSPVNLPEELRR	120				
Db	61	TCAAFCSRSLSCRKQKGFYDHLRDCISCAISCGQHPKQCAVFCENKLRSPVNLPEELRR	120				
Qy	121	QRSGEVNNSDNGRYOGLERHGSASPALPGLKLSADQVALVYST	166				
Db	121	QRSGEVNNSDNGRYOGLERHGSASPALPGLKLSADQVALVYST	166				
RESULT 8							
AA71914	ID	AA71914 standard;	Protein; 293 AA.				
XX	AC	AA71914;					
XX	DE	26-MAR-2001 (first entry)					
XX	DE	Human tumour necrosis factor receptor (TACI) protein.					
XX	KW	Human; transmembrane activator and CAML interactor; TACI;					
XX	KW	tumour necrosis factor receptor; TNF; autoimmune disease; diabetes;					
XX	KW	calcium-signal modulating cyclophilin ligand; CAML; viral infection;					
XX	KW	neurotrophin alpha polypeptide; TACI-Ligand; TACI-L; cytostatic; therapy;					
XX	KW	antiarthritic; antirheumatic; immunosuppressive; multiple sclerosis;					
XX	KW	rheumatoid arthritis; graft rejection; inflammation; cell proliferation;					
XX	KW	cell death; immunoglobulin E-mediated allergic reaction; IGE.					
XX	OS	Homo sapiens.					
XX	PH	Key	Location/Qualifiers				
XX	FT	Domain	2..166				
XX	FT		/label= Extracellular domain				
XX	FT		/note= "Binds with amino acids 123-285 of extracellular				
XX	FT		domain of TACI-L"				
XX	PN	WO200067034-A1.					
XX	PD	09-NOV-2000.					
XX	PP	14-APR-2000; 2000WO-US10282.					
XX	PR	30-APR-1999; 99US-0302863.					
XX	PA	(IMMU) IMMUNEX CORP.					
XX	PI	Goodwin RG, Din WS;					
XX	PI	WPI; 2001-016005/02.					
XX	DR	N-PSDB; AAD02006.					
XX	PT	Use of new interactions between tumour necrosis factor receptors (TACI)					
XX	PT	and TACI ligands to screen candidate molecules for determining agonist					
XX	PT	and antagonist interactions which are used for treating inflammation -					
XX	PS	Claim 10; Fig 1b; 46pp; English.					
XX	CC	The present sequence is a human tumour necrosis factor receptor (TACI)					
XX	CC	protein. TACI (transmembrane activator and calcium-signal modulating					
XX	CC	cyclophilin ligand (CAML)-interactor) forms a complex with neurotrophin					
XX	CC	alpha polypeptide (TACI-Ligand). The antagonist or agonist of					
XX	CC	TACI/TACI-L complex is useful for modulating an intracellular signalling					
XX	CC	cascade mediated by TACI/TACI-L complex. Antagonists of TACI/TACI-L					
XX	CC	complex are used to inhibit the interaction between TACI and TACI-L for					
XX	CC	therapeutic purposes to treat tumour and tumour metastasis and to combat					
XX	CC	various autoimmune diseases e.g. multiple sclerosis and diabetes, as					

CC well as other disorders, such as viral infection, rheumatoid arthritis,
 CC graft rejection, and immunoglobulin (Ig) E-mediated allergic reactions
 CC and inflammation. The interaction is used to study cellular processes
 CC associated with tumour necrosis factor (TNF)-receptors such as immune
 CC regulation, cell proliferation, cell death and inflammatory responses.
 CC The interaction between the extracellular region of TACI and TACI-L can
 CC be used to further develop understanding of which cell types TACI-L
 CC acts upon.

CC Sequence 293 AA;

Query Match 100.0%; Score 909; DB 22; Length 293;
 Best Local Similarity 100.0%; Pred. No. 5.6e-83;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGIGRRRRGRRVDOERFPQGLMTGVAMRSCPEEOYMDPLGTGCMSCKTICNHOSR 60
 DB 1 MSGIGRRRRGRRVDOERFPQGLMTGVAMRSCPEEOYMDPLGTGCMSCKTICNHOSR 60
 QY 61 TCAAFCRSLSCRKEQKRYDHLRLDCISCAISICGHPKQCAVFCENKLRSPVNLPEELRR 120
 DB 61 TCAAFCRSLSCRKEQKRYDHLRLDCISCAISICGHPKQCAVFCENKLRSPVNLPEELRR 120
 QY 121 QRSGEVENNSDNGRYQGLFHRGSEASPALPGLKLSADQVALVYST 166
 DB 121 QRSGEVENNSDNGRYQGLFHRGSEASPALPGLKLSADQVALVYST 166

RESULT 9

AAU99512
 ID AAU99512 standard; Protein; 293 AA.

AC AAU99512;

DT 07-OCT-2002 (first entry)

DE Human TACI-IgG Fc fusion protein.

KW Human; tumour necrosis factor; TNF delta; pulmonary system disorder;
 KW immunoglobulin production; B-cell proliferation; immune system disorder;
 KW autoimmune disease; cancer; lymphoproliferative disorder; pain;
 KW microbial infection; parasitic infection; bone disease; atherosclerosis;
 KW cardiovascular disorder; neurodegenerative disease; wound healing;
 KW graft versus host disease; haematopoietic cell disorder; nephritis;
 KW transmembrane activator and CAML-interactor; TACI; TNF epsilon; IgG;
 KW immunoglobulin G; Fc portion.

OS Homo sapiens.

PN US2002064829-A1.

PD 30-MAY-2002.

PE 14-JUN-2001; 2001US-0879919.

PR 14-MAR-1996; 96US-016812P.
 PR 15-JUN-2000; 2000US-211537P.
 PR 23-OCT-2000; 2000US-241952P.
 PR 13-DEC-2000; 2000US-254875P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 23-MAR-2001; 2001US-277978P.
 PR 25-MAY-2001; 2001US-293499P.
 PR 12-MAR-1997; 97US-0815783.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Yu G, Ni J, Gentz RL, Dillon PJ;

DR WPI; 2002-556722/59.

PT Novel human multimeric tumour necrosis factor delta or epsilon protein
 PT useful for treating disease or disorder of immune system such as
 PT autoimmune disease, immunodeficiency, or cancer of immune system -

XX Example 29; Page 125; 143pp; English.

PS The present invention relates to the isolation of human tumour necrosis
 XX factor (TNF) delta and TNF epsilon proteins, and the polynucleotide
 CC sequences encoding them. The proteins are useful for modulating
 CC immunoglobulin production or for modulating proliferation of B-cells.
 CC The sequences of the invention are useful for treating diseases or
 CC disorders of the immune system. Such disorders include autoimmune
 CC diseases (e.g. systemic lupus erythematosus (SLE), acquired
 CC immunodeficiency syndrome (AIDS)), cancers of the immune system
 CC (e.g. chronic lymphocytic leukaemia (CLL), multiple myeloma,
 CC non-Hodgkin's lymphoma or Hodgkin's disease), lymphoproliferative
 CC disorders, microbial infections (e.g. viral, bacterial), parasitic
 CC infections, nephritis, bone disease (e.g. osteoporosis), atherosclerosis,
 CC pain, cardiovascular disorders (e.g. myocardial infarction, stroke),
 CC neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's
 CC disease), graft versus host disease, wound healing, haematopoietic cell
 CC disorders (e.g. anaemia), inflammatory disorders (e.g. asthma),
 CC diseases or disorders associated with various mucous membranes of the
 CC body (e.g. mucositis), and disorders of the pulmonary system. The
 CC proteins are also useful as a vaccine adjuvant that enhances immune
 CC responsiveness to specific antigens. The present sequence for human
 CC transmembrane activator and CAML-interactor (TACI)-immunoglobulin G
 CC (IgG) Fc fusion protein is used in the examples of the present
 CC invention.

XX Sequence 293 AA;

Query Match 100.0%; Score 909; DB 23; Length 293;
 Best Local Similarity 100.0%; Pred. No. 5.6e-83;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGIGRRRRGRRVDOERFPQGLMTGVAMRSCPEEOYMDPLGTGCMSCKTICNHOSR 60
 DB 1 MSGIGRRRRGRRVDOERFPQGLMTGVAMRSCPEEOYMDPLGTGCMSCKTICNHOSR 60
 QY 61 TCAAFCRSLSCRKEQKRYDHLRLDCISCAISICGHPKQCAVFCENKLRSPVNLPEELRR 120
 DB 61 TCAAFCRSLSCRKEQKRYDHLRLDCISCAISICGHPKQCAVFCENKLRSPVNLPEELRR 120
 QY 121 QRSGEVENNSDNGRYQGLFHRGSEASPALPGLKLSADQVALVYST 166
 DB 121 QRSGEVENNSDNGRYQGLFHRGSEASPALPGLKLSADQVALVYST 166

RESULT 10

ABB81488
 ID ABB81488 standard; Protein; 293 AA.

AC ABB81488;

DT 02-SEP-2002 (first entry)

DE Human TACI receptor related protein SEQ ID NO:8.

KW Human; Znfir12; tumour necrosis factor receptor; cytosolic;
 KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;
 KW neuroprotective; antirheumatic; antiarthritic; antiaesthetic;
 KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
 KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
 KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
 KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
 KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
 KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;
 KW light chain neuropathy; hypertension; large vessel disease;
 KW graft-versus host disease; graft rejection; Crohn's disease.

OS Homo sapiens.

PN WO200238766-A2.

PD 16-MAY-2002.

XX 05-NOV-2001; 2001WO-US47018.
 PF
 XX 07-NOV-2000; 2000US-246449P.
 PR 20-DEC-2000; 2000US-257131P.
 PR 28-JUN-2001; 2001US-301715P.
 PR 29-AUG-2001; 2001US-315565P.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 PI Gross JA, Xu W, Renne RM, Grant FU;
 XX
 XX WPI: 2002-508212/54.
 DR
 XX
 XX Novel isolated human tumor necrosis factor receptor polypeptide, termed
 PT Znf12, useful for treating autoimmune disorders, emphysema, end
 PT stage renal failure or renal disease and lymphoma
 XX
 XX
 PS Disclosure; Page 136-137; 154pp; English.
 XX
 XX The present invention describes a human tumour necrosis factor receptor
 CC designated Znf12 (I). (I) has cytostatic, immunosuppressive,
 CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
 CC antineumatic, antiarthritic, antiaesthetic, nephrotropic and hypotensive
 CC activities, and can be used in gene therapy. (I) can be used for
 CC inhibiting, in a mammal, the activity of a ligand that binds Znf12
 CC (e.g. ZNF14), for treating disorders and diseases associated with B
 CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
 CC inhibiting the proliferation of tumour cells. (I) is useful for treating
 CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
 CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
 CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
 CC leukaemia, nephritis, and pyelonephritis, and for treating renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
 CC amyloidosis, hyperkalemia, large vessel diseases, graft-versus host
 CC disease, graft rejection and Crohn's disease. (I) is useful for
 CC modulating the immune system, for regulating B cell responses and
 CC development, for modulating development of other cells, antibody
 CC production and cytokine production, and for modulating T and B cell
 CC communication. The present sequence represents a protein which is
 CC given in the exemplification of the present invention.
 XX
 SQ Sequence 293 AA;
 Query Match 100.0%; Score 909; DB 23; Length 293;
 Best Local Similarity 100.0%; Pred. No. 5.6e-83;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSGGSRSGRRGSRVDOERFPQGLMTGVAMRSCPEBOYMDPLGTGMSCKTICNHOSOR 60
 DB 1 MSGGSRSGRRGSRVDOERFPQGLMTGVAMRSCPEBOYMDPLGTGMSCKTICNHOSOR 60
 QY 61 TCAAFCRSLSCRKQKGYDHLRDCISCASICGQHPKQCAVFCENKLRSPVNPPELRR 120
 DB 61 TCAAFCRSLSCRKQKGYDHLRDCISCASICGQHPKQCAVFCENKLRSPVNPPELRR 120
 QY 121 QRSGEVENNSDNGRYOGLFHRGSEASPALPGLKLSADQVALVYST 166
 DB 121 QRSGEVENNSDNGRYOGLFHRGSEASPALPGLKLSADQVALVYST 166
 RESULT 11
 AA014130
 ID AA014130 standard; Protein; 293 AA.
 XX
 XX AA014130;
 AC
 XX
 DT 02-MAY-2002 (first entry)
 XX
 DE Human transmembrane activator CAML interactor protein (TACI).
 XX Human transmembrane activator CAML interactor protein; TACI; cytosstatic;

KW cell proliferation; tumour; vulnery; renal cell cancer; mastocytoma;
 KW Kaposi's sarcoma; breast; ovarian carcinoma; rectal; throat; melanoma;
 KW colon; bladder; mammary adenocarcinoma; gastrointestinal; hyperplasia;
 KW pharyngeal squamous cell; stomach; cellular hyperproliferation; pannus;
 KW scleroderma; rheumatoid arthritis; scarring; liver; lung fibrosis;
 KW uterine.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..114
 FT /label= Extracellular_domain
 XX
 XX MO200181417-A2.
 XX
 XX 01-NOV-2001.
 PD
 XX
 XX 27-APR-2001; 2001WO-US40626.
 PF
 XX
 XX 27-APR-2000; 2000US-199946P.
 PR
 XX
 XX (BIOJ) BIOGEN INC.
 PA (APOT-) APOTEC R & D SA.
 PA
 PI Ambrose C, Thompson J, Schneider P, Rennett P;
 XX
 XX WPI: 2002-062027/08.
 DR N-PSDB; AAK98726.
 DR
 XX
 XX Treating mammal for condition associated with undesired cell
 PT proliferation e.g., solid tumour or reducing solid tumour size located in
 PT mammal comprises administering transmembrane activator CAML interactor
 PT protein reagent -
 XX
 PS Claim 8; Fig 1; 42pp; English.
 XX
 XX This sequence represents the human transmembrane activator CAML
 CC interactor protein (TACI). The invention relates to treating a mammal for
 CC a condition associated with undesired cell proliferation (e.g. a solid
 CC tumour, or reducing the size of a solid tumour located on or in a mammal)
 CC comprising administering a transmembrane activator CAML interactor
 CC protein (TACI) reagent. The TACI reagent has cytostatic and vulnery
 CC activity. Treating a mammal (e.g. human, cow, horse, dog, mouse, rat or
 CC cat) for a condition associated with undesired cell proliferation (e.g.
 CC sarcoma, ovarian carcinoma, rectal cancer, throat cancer, melanoma, colon
 CC cancer, bladder cancer, mastocytoma, lung cancer, mammary adenocarcinoma,
 CC pharyngeal squamous cell carcinoma, gastrointestinal cancer or stomach
 CC cancer). The method is also useful for treating cellular
 CC hyperproliferation (hyperplasia) such as scleroderma, pannus formation in
 CC rheumatoid arthritis, post-surgical scarring and lung, liver and uterine
 CC fibrosis. The TACI reagent of the invention can extend mean survival time
 CC of a mammal by 25% as compared to the mean survival time of a mammal in
 CC the absence of administering the TACI reagent. The TACI reagent also
 CC reduces the size of the tumour by 25% or more.
 XX
 SQ Sequence 293 AA;
 Query Match 100.0%; Score 909; DB 23; Length 293;
 Best Local Similarity 100.0%; Pred. No. 5.6e-83;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSGGSRSGRRGSRVDOERFPQGLMTGVAMRSCPEBOYMDPLGTGMSCKTICNHOSOR 60
 DB 1 MSGGSRSGRRGSRVDOERFPQGLMTGVAMRSCPEBOYMDPLGTGMSCKTICNHOSOR 60
 QY 61 TCAAFCRSLSCRKQKGYDHLRDCISCASICGQHPKQCAVFCENKLRSPVNPPELRR 120
 DB 61 TCAAFCRSLSCRKQKGYDHLRDCISCASICGQHPKQCAVFCENKLRSPVNPPELRR 120
 QY 121 QRSGEVENNSDNGRYOGLFHRGSEASPALPGLKLSADQVALVYST 166
 DB 121 QRSGEVENNSDNGRYOGLFHRGSEASPALPGLKLSADQVALVYST 166

RESULT 12
AAU75408
ID AAU75408 standard; Protein; 293 AA.
XX
AC AAU75408;
XX
DT 09-APR-2002 (first entry)
XX
DE Tumour necrosis factor (TNF) receptor TACI-Fc fusion.
XX
KM Tumour necrosis factor; TNF; cytostatic; arteriosclerosis;
KM analgesic; cerebroprotective; neurotrophic; hepatotropic;
KM immunoglobulin production; B cell proliferation; immunosuppressive;
KM HIV; human immunodeficiency virus; autoimmune disease; immunodeficiency;
KM Sjogren's syndrome; systemic lupus erythematosus; Hodgkin's disease;
KM common variable immunodeficiency; CVID; non-Hodgkin's lymphoma; AIDS;
KM acquired immunodeficiency virus; cancer; multiple myeloma; CLL;
KM chronic lymphocytic leukaemia; lymphoproliferative disorder;
KM bacterial infection; viral infection; osteoporosis; atherosclerosis;
KM pain; cardiovascular disorder; stroke; allergy; Alzheimer's disease;
KM neurodegenerative disease; inflammation; liver disease; cirrhosis;
KM cardiomyopathy; diabetes; asthma; psoriasis; glomerulonephritis;
KM ulcerative colitis; angiogenesis; septic shock; wound healing;
KM tumour necrosis factor receptor; TACI; immunoglobulin; IgG.
XX
OS Homo sapiens.
XX Synthetic.
XX WO200196528-A2.
XX
XX PD 20-DEC-2001.
XX
XX PF 14-JUN-2001; 2001WO-US19026.
XX
XX PR 15-JUN-2000; 2000US-211537P.
XX PR 23-OCT-2000; 2000US-241952P.
XX PR 13-DEC-2000; 2000US-254875P.
XX PR 16-MAR-2001; 2001US-276248P.
XX PR 23-MAR-2001; 2001US-277978P.
XX PR 25-MAY-2001; 2001US-293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX PA Yu G, Ni J, Gentz RL, Dillon PJ, Hilbert D;
XX
XX WPI, 2002-130727/17.
XX
XX DR N-PSDB; ABK13415.
XX
XX PT Novel multimeric human tumour necrosis factor delta or epsilon protein
XX PT useful for treating cancer, immune system disorder, infection,
XX PT cardiovascular disorders, liver disease, cardiomyopathy, diabetes and
XX PT psoriasis -
XX
XX Example 29; Page 341-342; 344pp; English.
XX
XX PS The invention describes a multimeric human tumour necrosis factor (TNF)
XX CC delta or epsilon protein (I). (I) or a composition containing them (II)
XX CC are useful for modulating immunoglobulin production or proliferation of B
XX CC cells. (I) or (II) is useful for treating a disease or disorder of the
XX CC immune system, preferably an autoimmune disease (e.g. Sjogren's syndrome,
XX CC systemic lupus erythematosus or common variable immunodeficiency (CVID));
XX CC an immunodeficiency e.g. acquired immunodeficiency syndrome (AIDS);
XX CC cancer of the immune system (e.g. Hodgkin's disease, non-Hodgkin's
XX CC lymphoma, multiple myeloma and chronic lymphocytic leukaemia (CLL)); in
XX CC the diagnosis and treatment or prevention of cancer, lymphoproliferative
XX CC disorder, bacterial and viral infections, osteoporosis, atherosclerosis,
XX CC pain, cardiovascular disorders (e.g. stroke), allergy, inflammation,
XX CC neurodegenerative disease (e.g. Alzheimer's disease), liver disease (e.g.
XX CC cirrhosis), cardiomyopathy, diabetes, asthma, psoriasis, septic shock,
XX CC glomerulonephritis, ulcerative colitis, arteriosclerosis, for promoting
XX CC angiogenesis and wound healing; as a diagnostic research reagent; as an

CC agent to target and kill cells expressing a TNFdelta and/or TNFepsilon
CC receptor; in apoptosis of transformed cell lines; mediation of cell
CC activation and proliferation; and as an immunogen to produce (ii). (iii)
CC is useful to purify, detect and target (I), for measuring levels of (I)
CC in biological samples, for immunophenotyping samples, and to treat,
CC inhibit or prevent diseases and disorders associated with aberrant
CC expression and/or activity of (I). This is the amino acid sequence of a
CC fusion protein of tumour necrosis factor receptor TACI and immunoglobulin
CC G (IgG) crystallisation fragment, described in the method of the
CC invention.
XX
XX SQ Sequence 293 AA;
XX
XX Query Match 100.0%; Score 909; DB 23; Length 293;
XX Best Local Similarity 100.0%; Pred. No. 5.6e-83;
XX Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MSGGLRSRRGSRVDOERPPQGLMTGVNARSCEBEQYMPDLGTCSCKTICNHQSOR 60
XX DB 1 MSGGLRSRRGSRVDOERPPQGLMTGVNARSCEBEQYMPDLGTCSCKTICNHQSOR 60
XX QY 61 TCAAFCRSLSCREKQKRYDHLRDCISCAISCGQHPKQCAVFCENKLRSPVNLPPELRR 120
XX DB 61 TCAAFCRSLSCREKQKRYDHLRDCISCAISCGQHPKQCAVFCENKLRSPVNLPPELRR 120
XX QY 121 QRSGEVENNSDNGRYQGLERHGSSEAPLPGLKLSADQVALVYST 166
XX DB 121 QRSGEVENNSDNGRYQGLERHGSSEAPLPGLKLSADQVALVYST 166
XX
XX RESULT 13
XX AAEL5493
XX ID AAEL5493 standard; Protein; 293 AA.
XX
XX AC AAEL5493;
XX
XX DT 12-MAR-2002 (first entry)
XX
XX DE Human transmembrane activator and intracellular CAML interactor protein.
XX
XX KM Human; transmembrane activator and intracellular CAML interactor; TACT;
XX KM cytoskeletal; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
XX KM lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
XX KM prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
XX KM drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
XX KM Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
XX KM human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
XX KM rheumatoid arthritis; atherosclerosis.
XX
XX OS Homo sapiens.
XX
XX PH Key location/Qualifiers
XX FT 34..66 /note= "Cysteine-rich consensus region"
XX FT 71..104 /note= "Cysteine-rich consensus region"
XX FT 167..186 /label= Transmembrane_domain
XX FT Domain
XX
XX WO200187979-A2.
XX
XX PN 22-NOV-2001.
XX
XX PD 14-MAY-2001; 2001WO-US15567.
XX
XX PR 12-MAY-2000; 2000US-204039P.
XX PR 27-JUN-2000; 2000US-214591P.
XX PR 14-MAY-2001; 2001US-0214591.
XX
XX PA (AMGE-) AMGEN INC.
XX
XX Theill LE, Yu G;
XX

DR WPI: 2002-066686/09.
 XX Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand -
 XX
 XX Disclosure; Fig 12A, 94pp; English.
 XX
 CC The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human TACI protein.
 XX
 SQ Sequence 293 AA;
 Query Match 100.0%; Score 909; DB 23; Length 293;
 Best Local Similarity 100.0%; Pred. No. 5.6e-83;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSGGSRSGRGRSVDOEREPQGLMTGVAMRSCPEBOYMDPLGTGMSCKTICNHQSOR 60
 DB 1 MSGGSRSGRGRSVDOEREPQGLMTGVAMRSCPEBOYMDPLGTGMSCKTICNHQSOR 60
 QY 61 TCAACRSLSCRKKEGKRYDHLNRDCISCAISCGHPKQCAVFCENKLRSPVNLPEELRR 120
 DB 61 TCAACRSLSCRKKEGKRYDHLNRDCISCAISCGHPKQCAVFCENKLRSPVNLPEELRR 120
 QY 121 QRSGEVNNSDNSGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166
 DB 121 QRSGEVNNSDNSGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166
 RESULT 14
 AAU09900 standard; Protein; 293 AA.
 AC AAU09900;
 DT 12-MAR-2002 (first entry)
 XX
 XX Human AGP-3 related protein receptor.
 XX
 KW Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive;
 KW dermatological; neuroprotective; nootropic; immunomodulator; metabolic;
 KW antidiabetic; analgesic; nephrotropic; osteopathic; cytotoxic; fever;
 KW antiparkinsonian; antipneumatic; vasotropic; antibacterial; asthma;
 KW AGP-3 receptor; tumor necrosis factor ligand family; AGP-3 receptor;
 KW meenteric lymph node; AGP-3R; inflammatory disease; immune disorder;
 KW rheumatoid arthritis; graft-versus-host disease; Crohn's disease;
 KW pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease;
 KW diabetes; glomerulonephritis; inflammatory bowel disease; ischemia;
 KW multiple sclerosis; Parkinson's disease; transgenic animal.
 XX
 OS Homo sapiens.
 XX
 XX WO200185782-A2.

PD 15-NOV-2001.
 XX
 XX 12-FEB-2001; 2001WO-US04568.
 XX
 PR 11-FEB-2000; 2000US-181800P.
 XX
 PA (AMGE-) AMGEN INC.
 PI Boyle WJ, Heu H;
 XX
 DR WPI: 2002-049441/06.
 DR N-PSDB; AAS18558.
 XX
 XX Composition, useful for identifying modulator of receptor for treating
 PT asthma and glomerulonephritis, comprises AGP-3 (tumor necrosis factor
 PT ligand family member) receptor and encoding nucleic acids -
 XX
 XX Disclosure; Page 117-119, 124pp; English.
 XX
 PS The invention relates to a composition (I) comprising AGP-3 receptor
 CC (tumor necrosis factor ligand family member) related protein (II)
 CC attached to a vehicle protein. (I) is useful for modulating AGP-3-related
 CC activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in
 CC assays to identify cells and tissues that express AGP-3R or proteins
 CC related to AGP-3R-related protein and for identifying compounds
 CC (agonists or antagonists) that interact with AGP-3R proteins. (II) is
 CC also useful for identifying intracellular proteins that interact with
 CC the respective cytoplasmic domains by yeast two-hybrid screening
 CC process. (II) is involved in B cell growth, survival and activation
 CC particularly in lymph node, spleen, and Peyer's patches. AGP-3R
 CC agonists and antagonists identified using (II) are used for modulating
 CC B cell response and are used to treat diseases characterised by
 CC inflammatory processes or deregulated immune response such as
 CC rheumatoid arthritis, graft-versus-host disease, Crohn's disease,
 CC lupus, etc. (II) is also useful in the production of hybridoma cells
 CC which are derived from B cells, which involves treating the hybridoma
 CC cells with (II). (II) is useful in the treatment of inflammatory
 CC conditions of joints, e.g., rheumatoid arthritis, osteoarthritis, etc.
 CC (II), its agonists or antagonists are useful for treating acute
 CC pancreatitis, amyotrophic lateral sclerosis (ALS), Alzheimer's disease,
 CC asthma, atherosclerosis, cachexia/anorexia, diabetes, fever,
 CC glomerulonephritis, inflammatory bowel disease, ischemic injury
 CC including cerebral ischemia, multiple myeloma, multiple sclerosis,
 CC osteoporosis, Parkinson's disease, pain, reperfusion injury, septic
 CC shock, etc. The nucleic acids are also useful for developing transgenic
 CC animals expressing (II), which are useful for producing the polypeptides
 CC and for the study of in vivo biological activity. The present sequence
 CC represents the amino acid sequence of human AGP-3 related protein
 CC receptor.
 XX
 SQ Sequence 293 AA;
 Query Match 100.0%; Score 909; DB 23; Length 293;
 Best Local Similarity 100.0%; Pred. No. 5.6e-83;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSGGSRSGRGRSVDOEREPQGLMTGVAMRSCPEBOYMDPLGTGMSCKTICNHQSOR 60
 DB 1 MSGGSRSGRGRSVDOEREPQGLMTGVAMRSCPEBOYMDPLGTGMSCKTICNHQSOR 60
 QY 61 TCAACRSLSCRKKEGKRYDHLNRDCISCAISCGHPKQCAVFCENKLRSPVNLPEELRR 120
 DB 61 TCAACRSLSCRKKEGKRYDHLNRDCISCAISCGHPKQCAVFCENKLRSPVNLPEELRR 120
 QY 121 QRSGEVNNSDNSGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166
 DB 121 QRSGEVNNSDNSGRYQGLEHRSSEASPALPGLKLSADQVALVYST 166
 RESULT 15
 AA014135 standard; Protein; 312 AA.
 ID AA014135
 XX

AA014135;
02-MAY-2002 (first entry)
Protein of N-terminus FLAG-tagged human full length TACI from pJST552.
Human transmembrane activator CAML interactor protein; TACI; cytosolic;
cell proliferation; tumour; vulnery; renal cell cancer; mastocytoma;
Kaposi's sarcoma; breast; ovarian carcinoma; rectal; throat; melanoma;
colon; bladder; mammary adenocarcinoma; gastrointestinal; hyperplasia;
pharyngeal squamous cell; stomach; cellular hyperproliferation; pannus;
scleroderma; rheumatoid arthritis; scarring; mean survival time; liver;
lung fibrosis; uterine; a proliferation inducing ligand; N-terminus;
pJST552; APRIL-R2.
Homo sapiens.
Synthetic.
Key Location/Qualifiers
FT Misc-difference 302 /label= Xaa
FT /note= "Xaa is encoded by TAA"
WO200101417-A2.
01-NOV-2001.
27-APR-2001; 2001WO-US40626.
27-APR-2000; 2000US-199946P.
(BIOJ) BIOGEN INC.
PA (APOT-) APOTEC R & D SA.
Ambrose C, Thompson J, Schneider P, Rennett P;
WPI, 2002-062027/08.
N-PSDB; AAK98731.
Treating mammal for condition associated with undesired cell
proliferation e.g., solid tumour or reducing solid tumour size located in
mammal comprises administering transmembrane activator CAML interactor
protein reagent -
Example 1; Fig 2; 42pp; English.
This sequence represents the protein of an N-terminus FLAG-tagged human
full length TACI from pJST552 (FLAG-tagged human APRIL-R2 (a
proliferation inducing ligand)). The invention relates to treating a
mammal for a condition associated with undesired cell proliferation (e.g.
a solid tumour, or reducing the size of a solid tumour located on or in a
mammal) comprising administering a transmembrane activator CAML
interactor protein (TACI) reagent. The TACI reagent has cytostatic and
vulnerary activity. Treating a mammal (e.g. human, cow, horse, dog,
mouse, rat or cat) for a condition associated with undesired cell
proliferation (e.g. cancer such as renal cell cancer, Kaposi's sarcoma,
breast cancer, sarcoma, ovarian carcinoma, rectal cancer, throat cancer,
melanoma, colon cancer, bladder cancer, mastocytoma, lung cancer, mammary
adenocarcinoma, pharyngeal squamous cell carcinoma, gastrointestinal
cancer or stomach cancer). The method is also useful for treating
cellular hyperproliferation (hyperplasia) such as scleroderma, pannus
formation in rheumatoid arthritis, post-surgical scarring and lung, liver
and uterine fibrosis. The TACI reagent of the invention can extend mean
survival time of a mammal by 25% as compared to the mean survival time of
a mammal in the absence of administering the TACI reagent. The TACI
reagent also reduces the size of the tumour by 25% or more.

Sequence 312 AA;
SQ

Query Match 99.4%; Score 904; DB 23; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.9e-82;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SGI GSRSRGGRSRVDOEERFPOGLMTGVAMRSCPEEQYWDPLGTGMSCKTICNHQSORT 61
DB 10 SGI GSRSRGGRSRVDOEERFPOGLMTGVAMRSCPEEQYWDPLGTGMSCKTICNHQSORT 69
QY 62 CAAPCRSLSCREOGKRFYDHLIRDCISCASTIGCHPKOCAYFCENKLSPPVNLPEELRRQ 121
DB 70 CAAPCRSLSCREOGKRFYDHLIRDCISCASTIGCHPKOCAYFCENKLSPPVNLPEELRRQ 129
QY 122 RSGEVEYNNSDNSGRYQGLEHRSSEASPALPGIKLSADQVALVYST 166
DB 130 RSGEVEYNNSDNSGRYQGLEHRSSEASPALPGIKLSADQVALVYST 174

Search completed: February 4, 2003, 12:57:46
Job time : 44.3401 secs

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OM protein - protein search, using SW model

Run on: February 4, 2003, 12:53:41 / Search time 35.6194 Seconds
(without alignments)
960.257 Million cell updates/sec

Title: US-09-854-864-15

Perfect score: 909
Sequence: 1 MSGIGSRSGRGRVDOEER.....SPALPGKLSADQVALVYST 166

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_rhnc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_prodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriopl:*
- 17: sp_archaeopl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	140	15.4	156	6 Q9N146	Q9N146 macaca mula
2	93	10.2	840	4 Q96H26	Q96H26 homo sapien
3	93	10.2	1240	4 Q15030	Q15030 homo sapien
4	91	10.0	1704	5 Q94446	Q94446 chironomus
5	89	9.8	839	5 Q10652	Q10652 caenorhabdi
6	89	9.8	1878	4 Q9UIP9	Q9UIP9 homo sapien
7	88.5	9.7	665	5 Q9W241	Q9W241 drosophila
8	88.5	9.7	676	5 Q8SW8	Q8SW8 drosophila
9	87.5	9.6	415	4 Q8TCB8	Q8TCB8 homo sapien
10	87	9.6	272	4 Q9BXV4	Q9BXV4 homo sapien
11	86.5	9.5	310	10 Q03108	Q03108 homo sapien
12	86.5	9.5	353	10 Q03107	Q03107 triticum ae
13	86.5	9.5	1299	5 Q26489	Q26489 spodoptera
14	86	9.4	267	13 Q919M0	Q919M0 neoceratodu
15	85	9.4	1137	4 Q9H8C1	Q9H8C1 homo sapien
16	85	9.4			

17	85	9.4	1918	4 Q9BQM7	Q9BQM7 homo sapien
18	85	9.4	1925	4 Q9P2E3	Q9P2E3 homo sapien
19	84.5	9.3	355	16 Q8ZDV4	Q8ZDV4 yersinia pe
20	84.5	9.3	598	11 Q8R151	Q8R151 mus musculu
21	84.5	9.3	702	5 Q9VH96	Q9VH96 drosophila
22	83	9.1	820	10 Q9FFK8	Q9FFK8 arabidopsis
23	83	9.1	13288	6 Q18758	Q18758 sus scrofa
24	82.5	9.1	913	4 Q96BP4	Q96BP4 homo sapien
25	82.5	9.1	1362	13 Q9PVZ4	Q9PVZ4 xenopus lae
26	82	9.0	239	13 Q90ZL0	Q90ZL0 fuqu rubrip
27	82	9.0	868	5 Q9Y1V3	Q9Y1V3 polyandroca
28	82	9.0	932	11 Q6Z030	Q6Z030 mus musculu
29	82	9.0	1650	11 Q9QVT6	Q9QVT6 ratcus sp.
30	81.5	9.0	316	11 Q9Z2H9	Q9Z2H9 mus musculu
31	81	8.9	567	4 Q8WU13	Q8WU13 homo sapien
32	81	8.9	704	3 Q74567	Q74567 trichoderma
33	81	8.9	1140	4 Q96K7	Q96K7 homo sapien
34	80	8.8	108	16 Q07571	Q07571 bacillus su
35	80	8.8	330	5 Q18118	Q18118 caenorhabdi
36	80	8.8	996	11 Q924X6	Q924X6 mus musculu
37	80	8.8	1664	5 Q9TVQ2	Q9TVQ2 caenorhabdi
38	80	8.8	1792	13 Q57484	Q57484 gallus gall
39	79.5	8.7	98	5 Q16939	Q16939 arcylostroma
40	79.5	8.7	593	10 Q9SEW4	Q9SEW4 juglans reg
41	79.5	8.7	1963	5 Q9VY56	Q9VY56 drosophila
42	79.5	8.7	2189	5 Q9BI05	Q9BI05 elimeria ten
43	79	8.7	217	11 Q9CSB2	Q9CSB2 mus musculu
44	79	8.7	269	17 Q29751	Q29751 archaeoglob
45	79	8.7	317	11 Q70524	Q70524 cricetus

ALIGNMENTS

RESULT 1	
Q9N146	PREDIMINARY; PRT; 156 AA.
ID Q9N146	
AC Q9N146	
DT 01-OCT-2000 (TREMBLrel. 15, Created)	
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)	
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)	
DE Transmembrane activator (Fragment).	
GN NF-AT.	
OS Macaca mulatta (Rhesus macaque).	
OC Eukaryota; Metazoa; Chordata; Vertebrata; Buteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;	
OC Cercopitheidae; Macaca.	
OX NCBI_TaxID=9544;	
RN [1]	
RP SEQUENCE FROM N.A.	
RA Arredondo J;	
RT "Cytokine Signal Transduction Genes from Rhesus Macaque";	
RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.	
DR EMBL; AF227558; AAF73400.1; -.	
FT NON TER	
FT SEQUENCE 156 AA; 16170 MW; 8AD74E4D17D511D0 CRC64;	
Q96H26	
Query Match	15.4%; Score 140; DB 6; Length 156;
Best Local Similarity	96.6%; Pred. No. 6.1e-08;
Matches 28; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
Q96H26	
138 GLEHRSRSPALPGKLSADQVALVYST 166	
1 GLEHRSRSPALPGKLSADQVALVYST 29	
DB	
RESULT 2	
Q96H26	PREDIMINARY; PRT; 840 AA.
ID Q96H26	
AC Q96H26	
DT 01-DEC-2001 (TREMBLrel. 19, Created)	
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)	
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)	

DE Similar to bromodomain adjacent to zinc finger domain, 2A
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC008965; AAH08965.1; -
 DR InterPro; IPR000637; AT_hook.
 DR InterPro; IPR001487; Bromodomain.
 DR InterPro; IPR001965; Znf_PHD.
 DR Pfam; PF02178; AT_hook; 2.
 DR Pfam; PF00439; bromodomain; 1.
 DR Pfam; PR00628; PHD; 1.
 DR PROSITE; PS50014; BROMODOMAIN_2; 1.
 FT NON_TER 1
 SQ SEQUENCE 840 AA; 94884 MW; 3F8147D9B7034B45 CRC64;

Query Match 10.2%; Score 93; DB 4; Length 840;
 Best Local Similarity 25.8%; Pred. No. 0.086;
 Matches 40; Conservative 17; Mismatches 68; Indels 30; Gaps 7;

QY 22 PGLMTGVAMRSCPEQYMDPLIGTMSCKTI--CNHQSORTCA-----AFGRSLSCR 72
 DB 561 PEGTTTSEIETPRIRWRQTLERCRSAQVCLIGQLERSIAWEKSVNRYTC--LVCR 618
 QY 73 KEQKRYDHLRDCISCSAIGC---QHPKQCA-----YFC-----ENKLRSPVNLPP 116
 DB 619 KGDN---DEFLLCDCDRCGCHYCHRPMEAVPEGDWFCVCLAQVGEFTQKGFPEK 675
 QY 117 ELRQRSGEVENNSDNGRYQGLEHRSSEASPALP 151
 DB 676 RGQKRKSGYSLNFSBGDRRRRVLLRGRESPAACP 710

RESULT 3

015030 PRELIMINARY; PRT; 1240 AA.

AC 015030
 DT 01-JAN-1998 (TRENBLrel. 05, Created)
 DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE KIA00314 protein (Fragment).
 GN KIA00314.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRIN;
 RA MEDLINE=97349984; PubMed=9205841;
 RA Nagase T., Ishikawa K., Nakajima D., Ohira M., Seki N., Miyajima N.,
 RA Tanaka A., Kocani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. VII.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro."
 RL DNA Reg. 4:141-150 (1997).
 DR EMBL; AB002312; BAA20773.1; -
 DR HSSP; Q92831; 1B91.
 DR InterPro; IPR000637; AT_hook.
 DR InterPro; IPR001487; Bromodomain.
 DR InterPro; IPR004022; DDT_dom.
 DR InterPro; IPR001965; Znf_PHD.
 DR Pfam; PF02178; AT_hook; 3.
 DR Pfam; PF00439; bromodomain; 1.
 DR Pfam; PR00291; DDT; 1.
 DR Pfam; PR00628; PHD; 1.
 DR PRINTS; PR00929; ATHOOK.

DR PRINTS; PR00503; BROMODOMAIN.
 DR SMART; SM00384; AT_hook; 3.
 DR SMART; SM00297; BROMO; 1.
 DR SMART; SM00249; PHD; 1.
 DR PROSITE; PS50014; BROMODOMAIN_2; 1.
 FT NON_TER 1
 SQ SEQUENCE 1240 AA; 140417 MW; 20BDBF1AA6BC5A1 CRC64;

Query Match 10.2%; Score 93; DB 4; Length 1240;
 Best Local Similarity 25.8%; Pred. No. 0.13;
 Matches 40; Conservative 17; Mismatches 68; Indels 30; Gaps 7;

QY 22 PGLMTGVAMRSCPEQYMDPLIGTMSCKTI--CNHQSORTCA-----AFGRSLSCR 72
 DB 961 PEGTTTSEIETPRIRWRQTLERCRSAQVCLIGQLERSIAWEKSVNRYTC--LVCR 1018
 QY 73 KEQKRYDHLRDCISCSAIGC---QHPKQCA-----YFC-----ENKLRSPVNLPP 116
 DB 1019 KGDN---DEFLLCDCDRCGCHYCHRPMEAVPEGDWFCVCLAQVGEFTQKGFPEK 1075
 QY 117 ELRQRSGEVENNSDNGRYQGLEHRSSEASPALP 151
 DB 1076 RGQKRKSGYSLNFSBGDRRRRVLLRGRESPAACP 1110

RESULT 4

094446 PRELIMINARY; PRT; 1704 AA.

AC 094446
 DT 01-FEB-1997 (TRENBLrel. 02, Created)
 DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE 220 kDa silk protein.
 GN SP220.
 OS Chironomus thummi (midge).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
 OC Chironomidae; Chironomidae; Chironominae; Chironomus.
 OX NCBI_TaxID=7154;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Salivary Gland;
 RA Case S.T., Cox C., Bell W.C., Hoffman R.T., Martin J., Hamilton R.;
 RT "Extraordinary conservation of cysteines among homologous Chironomus
 RT silk proteins sp185 and sp220."
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U54641; AAA9804.1; -
 DR InterPro; IPR004153; CKXCX_repeat.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000853; McIlhion_nemat.
 DR Pfam; PF03128; CKXCX; 69.
 DR PRINTS; PR00876; MTNEMATODE.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_2.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 SQ SEQUENCE 1704 AA; 185746 MW; 3A3F2024708F1E28 CRC64;

Query Match 10.0%; Score 91; DB 5; Length 1704;
 Best Local Similarity 21.4%; Pred. No. 0.32;
 Matches 31; Conservative 22; Mismatches 44; Indels 48; Gaps 7;

QY 32 RSCPEQYWD-----PLIGTC-----MSCKTICNHQ-----SQTCAAF 66
 DB 1357 QTCFAGQSWDSQTCQSCFATGKTAQFMCACQCKVCVQENCKSPKVPDQSCSCCQ 1416
 QY 67 -RSLSCRKEQ---GKFTYH-----LRLDCISCSAIGQHKKQ---AYF 103
 DB 1417 PKNMPPPGECTAGRTWDATCTEKATVPNCSPMVPDQATCGCKGKDKPKJADXYW 1476
 QY 104 ENKLRSPVNLPELRORSEVEN 128
 DB 1477 CDKQAVCSLPITQCPYSGQTN 1501

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RESULT 5
Q10652 PRELIMINARY; PRT; 839 AA.
AC Q10652;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Zinc finger protein CEZF.
GN CEZF.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodidae; Caenorhabditis.
OX NCB1_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=96003854; PubMed=7568208;
RA Saha V., Chaplin T., Gregorini A., Ayton P., Young B.D.;
RT "The leukemia-associated-protein (LAP) domain, a cysteine-rich motif,
RT is present in a wide range of proteins, including MLT, APL10, and MLT6
RT proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 92:9737-9741(1995).
CC -1- SIMILARITY: CONTAINS A CYS-RICH (PHD-FINGER) DOMAIN SIMILAR TO
CC THOSE FROM HAT1.1, MAIZE HOX1A AND PARSLER PRH.
DR EMBL; U20555; AAC46918.1; -.
DR InterPro; IPR001965; Znf_PHD.
DR Pfam; PF00628; PHD; 1.
DR SMART; SM00249; PHD; 2.
KW DNA-binding; zinc-finger; Metal-binding.
FT DOMAIN 8 54 CYS-RICH (PHD-FINGER).
FT ZN FING 619 655 LEUCINE ZIPPER.
FT ZN FING 127 151 POTENTIAL.
SQ SEQUENCE 839 AA; 89439 MW; AFEFFB9D1D5B48 CRC64;

Query Match 9.8%; Score 89; DB 5; Length 839;
Best Local Similarity 32.5%; Pred. No. 0.24;
Matches 27; Conservative 8; Mismatches 28; Indels 20; Gaps 5;

QY 34 CPEQYWPDLGTSCMSC-KTICNHSQRTCAFCRSLSCKRQKQKPYDHLRDCISCASI 92
DB 130 CNEEPNDKAKCA-CMSCKSTCKRSHYTCAG-RKGLC--EEGAL----- 172
QY 93 CGQHPKQCAVFCENKLRSPVNP 115
DB 173 -SRNVKCGY-CENHLKKAINDP 193

RESULT 6
Q9UIF9 PRELIMINARY; PRT; 1878 AA.
AC Q9UIF9;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Bromodomain adjacent to zinc finger domain 2A.
GN BAZZA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20130112; PubMed=10662543;
RA Jones M.H., Hamana N., Nezu J., Shimane M.;
RT "A novel family of bromodomain genes."
RL Genomics 63:40-45(2000).
DR EMBL; AB032254; BAA89211.1; -.
DR HSSP; Q92831; 1891
DR InterPro; IPR000637; AT hook.
DR InterPro; IPR001487; Bromodomain.
DR InterPro; IPR004022; DDT_dom.
DR InterPro; IPR001739; Methyl-CpG_bind.
DR InterPro; IPR001965; Znf_PHD.

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DR Pfam; PF02178; AT_hook; 4.
DR Pfam; PF00439; bromodomain; 1.
DR Pfam; PF02791; DDT; 1.
DR Pfam; PF01429; MBP; 1.
DR Pfam; PF00628; PHD; 1.
DR PRINTS; PR00503; BROMODOMAIN.
DR SMART; SM00384; AT_hook; 3.
DR SMART; SM00297; BROMO; 1.
DR SMART; SM00391; MBP; 1.
DR SMART; SM00249; PHD; 1.
DR PROSITE; PS50014; BROMODOMAIN 2; 1.
SQ SEQUENCE 1878 AA; 208639 MW; 12683AFE63A93A6 CRC64;

Query Match 9.8%; Score 89; DB 4; Length 1878;
Best Local Similarity 23.3%; Pred. No. 0.61;
Matches 37; Conservative 18; Mismatches 66; Indels 38; Gaps 6;

QY 22 PGLMTGYANRSCPEQYWPDLGTSCSKTIC-----NHQSRTCAPFRS 68
DB 1599 PEGTTEISYEITPRIRIWRQTLQRCSAAHVCLGHLERSIAMEKSVNRYTC----- 1652
QY 69 LSCREKQKPYDHLRDCISCASITCG--QHPKQCA-----YFC-----ENKLRSPV 112
DB 1653 LVCRKGDN---DEFLLLDCDCDRGCHYCHRPKMEAVPEGWFTVCLAAQYVEGEFTQKP 1709
QY 113 NLPELPRQRSGEVENNSDNGRYOGLERHSGEASPALP 151
DB 1710 GPPKRGQKRGKGYSLNFESEGGRRRRVLLKGRSEPAAGP 1748

RESULT 7
Q9W241 PRELIMINARY; PRT; 665 AA.
AC Q9W241;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-OCT-2001 (TREMblrel. 18, Last annotation update)
DE CG12489 protein.
GN CG12489.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCB1_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Crawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieres S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gottrell J.H., Gu Z., Guan X., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hoeltin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaiswal M., Kalush F., Karen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laake P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Metkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

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RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reiert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spredling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtkac R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Massaman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
DR EMBL; AF03457; AAF46858.1; -
DR Flybase; FBgn0034738; CG12489.
DR InterPro; IPR000299; Band 4.1.
DR InterPro; IPR001641; Znf.Fing.
DR Pfam; PF00373; Band_41; 1.
DR SMART; SM00295; B41; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS50057; BAND_41_3; 1.
SQ SEQUENCE 665 AA; 71851 MW; D0281FPA5BA45683 CRC64;

Query Match 9.7%; Score 88.5; DB 5; Length 665;
Best Local Similarity 25.9%; Pred. No. 0.21;
Matches 43; Conservative 19; Mismatches 65; Indels 39; Gaps 9;

QY 2 SGIGRSRRGSRVDOEERFPQGLMTGVMRSCPEQYWDPLGTGMSCKTICNHQSORT 61
DB 499 TGAAGSMAG---KIDLAIREKA-----REAIERCVDTRISAMOCK-ICMDRAINT 547
QY 62 CAAFCSRLSCRKEQKFPYDHLRDCISASICGHPKQCAVFCENKLRSPVN--LPPELR 119
DB 548 VNPCC---C-----HVIA-CAQCAARCSNCPN-----CRVKTISVVKIYLPPELR 588
QY 120 RQRSGEVNNSDNGS-----RYGLEHRSASPALPGLKLSAD 158
DB 589 TSQTSGATTSSSIMDQVEQLLOQQLDEISAAPASLEAGAD 634

RESULT 8
Q8SWW8 PRELIMINARY; PRT; 676 AA.
AC Q8SWW8; 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE LD18186P.
GN CG12489.
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidae; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Agbayan A., Carlson J.,
RA Change M., Chavez C., Dorsett V., Drensek D., Farfan D., Friebe E.,
RA George R., Gonzalez M., Guatin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nuno J., Pacleb J., Pargass V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celisier S.;
RL Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY055032; AAM11360.1; -
SQ SEQUENCE 676 AA; 73182 MW; 8359E26A02CC087 CRC64;

Query Match 9.7%; Score 88.5; DB 5; Length 676;
Best Local Similarity 25.9%; Pred. No. 0.22;
Matches 43; Conservative 19; Mismatches 65; Indels 39; Gaps 9;
QY 2 SGIGRSRRGSRVDOEERFPQGLMTGVMRSCPEQYWDPLGTGMSCKTICNHQSORT 61
DB 499 TGAAGSMAG---KIDLAIREKA-----REAIERCVDTRISAMOCK-ICMDRAINT 547

DB 510 TGAAGSMAG---KIDLAIREKA-----REAIERCVDTRISAMOCK-ICMDRAINT 558
QY 62 CAAFCSRLSCRKEQKFPYDHLRDCISASICGHPKQCAVFCENKLRSPVN--LPPELR 119
DB 559 VNPCC---C-----HVIA-CAQCAARCSNCPN-----CRVKTISVVKIYLPPELR 599
QY 120 RQRSGEVNNSDNGS-----RYGLEHRSASPALPGLKLSAD 158
DB 600 TSQTSGATTSSSIMDQVEQLLOQQLDEISAAPASLEAGAD 645

RESULT 9
Q8TCB8 PRELIMINARY; PRT; 415 AA.
AC Q8TCB8; 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical 45.2 kDa protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC022399; AAH2399.1; -
KM Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 415 AA; 45230 MW; 945069C1607D38B3 CRC64;

Query Match 9.6%; Score 87.5; DB 4; Length 415;
Best Local Similarity 23.8%; Pred. No. 0.16;
Matches 46; Conservative 25; Mismatches 71; Indels 51; Gaps 11;

QY 6 RSRRGSRVDOEERFPQGLMTGVMRSCPEQYWDPLGTGMSCKTICNHQSORT 59
DB 89 RGRG-----ENLFATIDEGMDVPLAMEEWHREHYNLSAATC-SPGQMGHYTVV 140
QY 60 --RTCAFCRLSCRKEQKFPYDHLRDCIS-----ASICGHP-----KCC--AYF 103
DB 141 WAKTERIGGSHFCCKLGVEERTNI--ELVCNVEPPNVAVKRYDGTGPPSCPSGYH 198
QY 104 CENKLRSPVNL-----PELRQRSGEVNNSDNGSRYGGL-----EHRGS 144
DB 199 CKNSLCEPIGSPEDAQDPLVLTAPSPRATBASDSRKMGTIPSSLATGIPALVTEVSGS 258
QY 145 EASPALPGLKLSA 157
DB 259 LATKALPAVERQA 271

RESULT 10
Q9BXV4 PRELIMINARY; PRT; 272 AA.
AC Q9BXV4; 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Thrombospondin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Mao Y., Xie Y., Zhou Z., Zhao W., Zhao S., Wang W., Huang Y., Wang S.,
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.

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RC TISSUE=PLACENTA;
RA Strauberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF251057; AA034947.1; -
DR EMBL; BC022367; AA022367.1; -
DR InterPro; IPR002174; Furin-like.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00090; tsp_1; 1.
DR SMART; SM00261; FU; 2.
DR PROSITE; PS00209; TSP1.1.
DR PROSITE; PS50092; TSP1.1.
SQ SEQUENCE 272 AA; 30928 MW; CACAEC6B7E781189 CRC64;

Query Match
Best Local Similarity 24.6%; Score 87; DB 4; Length 272;
Matches 42; Conservative 18; Mismatches 59; Indels 52; Gaps 11;

Qy 28 GVAMRSCPEBOYD--PLIGTCMSCKTICNHOSORTCAAFCSLSCKRQGFYDHL--- 82
Db 74 GVCSSCPGYGFRYPINCKTKCKADCD---TC--FNNKF--CTKCKSGFYHLGKC 125
Qy 83 LRDC-----ISCASI-----CGQHPQCAV--FCENKLRSPV----- 112
Db 126 LDCPBGLEANNHTECVSIHCEVSEMNPMSPCTKKGKTCGFKGTETRVREITIQHPSA 185
Qy 113 --NLPELRORSSEVENNSDNGR--YQGLEHR-----GSEASPALPGLK 154
Db 186 KGNLCPTNETRKTCTVQRKKCKQKGRKKRKRKRKKRKNKSGSKALIPDSK 236

RESULT 11
Q096K87 PRELIMINARY; PRT; 292 AA.
AC 096K87;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE CDNA FLJ14440 file, clone HEMBL1000915, weakly similar to
DE subtilisin-like protease PACE4 precursor (EC 3.4.21.-).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EMBRIO;
RA Isegai T., Oca T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
RT "NDO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK027346; BAB55051.1; -
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00090; tsp_1; 1.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS50092; TSP1.1.
SQ SEQUENCE 292 AA; 33243 MW; 01E2774AC3DA46F8 CRC64;

Query Match
Best Local Similarity 24.6%; Score 87; DB 4; Length 292;
Matches 42; Conservative 18; Mismatches 59; Indels 52; Gaps 11;

Qy 28 GVAMRSCPEBOYD--PLIGTCMSCKTICNHOSORTCAAFCSLSCKRQGFYDHL--- 82
Db 74 GVCSSCPGYGFRYPINCKTKCKADCD---TC--FNNKF--CTKCKSGFYHLGKC 125
Qy 83 LRDC-----ISCASI-----CGQHPQCAV--FCENKLRSPV----- 112
Db 126 LDCPBGLEANNHTECVSIHCEVSEMNPMSPCTKKGKTCGFKGTETRVREITIQHPSA 185

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Qy 113 --NLPELRORSSEVENNSDNGR--YQGLEHR-----GSEASPALPGLK 154
Db 186 KGNLCPTNETRKTCTVQRKKCKQKGRKKRKRKRKNKSGSKALIPDSK 236

RESULT 12
Q003108 PRELIMINARY; PRT; 310 AA.
AC 003108;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Catchpsin B (Fragment).
OS Triticum aestivum (wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticaceae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VAR. CHINESE SPRING;
RX MEDLINE=93258430; PubMed=1302642;
RA Cejudo F.J., Murphy G., Chino C., Baulcombe D.C.;
RT "A gibberellin-regulated gene from wheat with sequence homology to
RT catchpsin B of mammalian cells.";
RL Plant J. 2:937-948(1992).
DR EMBL; X66014; CAA46812.1; -
DR HSSP; P07689; IODO.
DR MEROPS; C01.049; -.
DR InterPro; IPR000668; Peptidase_C1.
DR InterPro; IPR001693; Shprot_acsite.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PR00705; PAPA1N.
DR Prodom; PD000158; Peptidase_C1; 1.
DR PROSITE; PS00138; THIOL_PROTEASE_CYS; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
KW Hydroxylase; Thiol protease.
FT NON TER 310
SQ SEQUENCE 310 AA; 33811 MW; 2DE6F3264B228C3 CRC64;

Query Match
Best Local Similarity 24.7%; Score 86.5; DB 10; Length 310;
Matches 36; Conservative 12; Mismatches 63; Indels 35; Gaps 5;

Qy 22 PQGLMTGVAMRSCPE-----EQYWDPLIGTCMSCKTICNHOSORTCAAFCSLSR 72
Db 80 PQGLAGVPIKIHPEMDLPKFFDARTQMS-----SCSTIGNILDGHCACAFPAVE 132
Qy 73 KEQGFYDHL-----LRDCISGASICGHPKQCAVFCENKLRSPVNLPELRORSSE 125
Db 133 ALQDRFCILHMSVSLSYNDLLAC-----CGFLCSGCGNGGYIISMRYPFRSGV 182
Qy 126 VENNNSDNGRYQGLEHRSSEASPALP 151
Db 183 VTRECDPYFDQTCQHPGCE--PAYP 206

RESULT 13
Q003107 PRELIMINARY; PRT; 353 AA.
AC 003107;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Catchpsin B (Fragment).
OS Triticum aestivum (wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticaceae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VAR. CHINESE SPRING;

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RX MEDLINE=93258430; PubMed=1302642; Baulcombe D.C.;
 RA Cejudo F.J.; Murphy G.; Chinoy C.;
 RT "A gibberellin-regulated gene from wheat with sequence homology to
 RL cathepsin B of mammalian cells";
 DR Plant J. 2:937-948 (1992).
 DR EMBL; X66013; CAA46811.1; -.
 DR HSSP; P07688; 10DQ.
 DR MEROPS; C01.049; -.
 DR InterPro; IPR000668; Peptidase_C1.
 DR InterPro; IPR000169; SHprot_acidte.
 DR Pfam; PF00112; Peptidase_C1.1.
 DR PRINTS; PR00705; PAPA1N_C1.1.
 DR ProDom; PD000158; Peptidase_C1.1.
 DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
 DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
 KW Hydroxylase; Thiol protease.
 FT NON TER
 SQ SEQUENCE 353 AA; 38355 MW; A10E7C84ED46E44 CRC64;

Query Match 9.5%; Score 86.5; DB 10; Length 353;
 Best Local Similarity 24.7%; Pred. No. 0.18;
 Matches 36; Conservative 12; Mismatches 63; Indels 35; Gaps 5;

QY 22 PGLMTGVAMRSCPE-----EYWDPLGTCMSCKTICNQSORTCAAFCSLSGR 72
 DB 80 PGLAGVAPKIKHPMDLPKPPARTQWS-----SCSTIGNILDGHCACWAFAYVE 132
 QY 73 KQSGKRYDHL-----LRDCTSCASICGHPKQCAFCENKLRSPVNLPELRORSGE 125
 DB 133 ALQDRCTHLNNSVSLSVNDLAC-----CGFLGSGNGGYPISAMRYFRSGV 182
 QY 126 VENNDSNGRYQGLEHRSSEASPALP 151
 DB 183 VTBECDPYFDQTCQHPGCE--PAYP 206

RESULT 14

Q26489 PRELIMINARY; PRT; 1299 AA.

AC Q26489;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Endoprotease furin.
 GN FURIN.
 OS Spodoptera frugiperda (Fall armyworm).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Noctuidae; Noctuidae; Amphipyrinae; Spodoptera.
 OX NCBI_TaxID=7108;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SF9;
 RA Cieplik M., Klenk H.;
 RT "Cloning and functional characterization of FURIN from Spodoptera
 frugiperda (SF9) cells";
 RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
 DR EMBL; Z68888; CAA93116.1; -.
 DR HSSP; Q9405; 1MPF.
 DR InterPro; IPR002174; Furin-like.
 DR InterPro; IPR000209; Peptidase_S8.
 DR Pfam; PF01483; P_1.
 DR Pfam; PF00082; Peptidase_S8; 1.
 DR PRINTS; PR00723; SUBTILISIN.
 DR ProDom; PD000717; P_domain; 1.
 DR SMART; SM00261; FU; 10.
 DR PROSITE; PS00136; SUBTILASE ASP; 1.
 DR PROSITE; PS00137; SUBTILASE HIS; 1.
 DR PROSITE; PS00138; SUBTILASE_SER; 1.
 KW Protease.
 SQ SEQUENCE 1299 AA; 142020 MW; 4C3799C7B8C572AB CRC64;

Query Match 9.5%; Score 86; DB 5; Length 1299;
 Best Local Similarity 25.0%; Pred. No. 0.87;
 Matches 39; Conservative 16; Mismatches 51; Indels 50; Gaps 9;

QY 22 PGLMTGVAMRSCPEQYWDPLGTCMSCKTICNQSORTCAAFCSLSCKRECKF--- 78
 DB 1104 PRFMDGGLCNECLSGQYDADTSGTCSRCDASC-----RTCSG-----PQOFECT 1148
 QY 79 -----YDHLRDCISASICG-----QHPKQCAFCENKLRSPVNLPELRORSGEVE 127
 DB 1149 TCSRPLRLIDRLNNQVPCSESGVNSTPPTDCC-CH-----PE-----NGECI 1192
 QY 128 NNSDSNGRYQGLEHRSSEASPALPGLKLSADQVALV 163
 DB 1193 NSS-VAGKRRIEMGALHTAPSAD-----AAPSVAIV 1223

RESULT 15

Q919M0 PRELIMINARY; PRT; 267 AA.

AC Q919M0;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Proenkephalin.
 OS Neoceratodus forsteri (Australian lungfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Dipnoi; Ceratodontiformes; Ceratodontidae; Neoceratodus.
 OX NCBI_TaxID=7892;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE=20417836; PubMed=10960597;
 RA Sollare C., Danielson P., Jose J.M.P., Does R.M.;
 RT "Deciphering the origin of Met-enkephalin and Leu-enkephalin in lobe-
 finned fish: cloning of Australian lungfish proenkephalin";
 RL Brain Res. 874:131-136 (2000).
 DR EMBL; AF232671; AAF44658.1; -.
 DR InterPro; IPR000094; Opioid neurop.
 DR Pfam; PF01160; Opioid neurop; 1.
 DR PRINTS; PR01028; OPTOIPRCSR.
 DR PROSITE; PS01252; OPTOIDS_PRECURSOR; UNKNOWN_1.
 SQ SEQUENCE 267 AA; 30688 MW; 69C92C0F3378E0F0 CRC64;

Query Match 9.4%; Score 85; DB 13; Length 267;
 Best Local Similarity 29.4%; Pred. No. 0.19;
 Matches 30; Conservative 7; Mismatches 35; Indels 30; Gaps 5;

QY 62 CAAFRSLSCKRECKRYDHLRDCISASICGQH---PKQCAFCENKLRSPVNSWDMC 110
 DB 15 CA--CLILAVRAECSK-----DCAHCTYHIGQADINPLSTLECGKLPVNSWDMC 65
 QY 111 ----PVNLPELRORSGEVENNSDN-----SGRYQLEHR 142
 DB 66 KELLQVGRPEIMQEGETASVENDKENDQRMFAKRYGGFMRR 107

Search completed: February 4, 2003, 12:59:11
 Job time : 38.6194 secs

GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: February 4, 2003, 12:53:16 ; Search time 11.4251 Seconds
(without alignments)
602.627 Million cell updates/sec

Title: US-09-854-864-15

Perfect score: 909
Sequence: 1 MSGIGRSRRGSRVDQER.....SPALPGKLSADQVALVYST 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query	Length	ID	Description
1	909	100.0	293	1	T13X_HUMAN
2	419.5	46.1	249	1	T13X_MOUSE
3	97.5	10.7	1877	1	PCK5_MOUSE
4	89	9.8	867	1	YMA2_CAEEL
5	86	9.5	297	1	XEDA_HUMAN
6	83	9.1	971	1	RECK_MOUSE
7	83	9.1	1150	1	APMU_PIG
8	82.5	9.1	913	1	PCK5_HUMAN
9	82	9.0	4660	1	LRP2_RAT
10	81	8.9	971	1	RECK_HUMAN
11	81	8.9	1124	1	TIER2_HUMAN
12	80.5	8.9	937	1	PAC4_RAT
13	79.5	8.7	1172	1	LMB3_HUMAN
14	79.5	8.7	1984	1	YL_DROME
15	78.5	8.6	630	1	2147_HUMAN
16	77.5	8.5	2871	1	PBN1_MOUSE
17	76.5	8.4	1680	1	PUR2_DROME
18	76	8.4	603	1	CPAI_MOUSE
19	76	8.4	1877	1	PCK5_PAT
20	75.5	8.3	427	1	YK15_YEAST
21	75	8.3	400	1	LMB_HIRME
22	75	8.3	446	1	FAT_MOUSE
23	75	8.3	448	1	EDAR_HUMAN
24	75	8.3	969	1	PAC4_HUMAN
25	75	8.3	2871	1	PBN1_HUMAN
26	75	8.3	4544	1	LRP1_MOUSE
27	74.5	8.2	501	1	TBA2_BOVIN
28	74.5	8.2	773	1	ITB1_BOVIN
29	74	8.1	1125	1	TIER2_BOVIN
30	74	8.1	1426	1	EGFR_DROME
31	74	8.1	2569	1	LMA3_MOUSE
32	73.5	8.1	775	1	PINC_MOUSE
33	73.5	8.1	798	1	ITB1_MOUSE

ALIGNMENTS

RESULT 1	ID	T13X_HUMAN	STANDARD	PRT	293 AA.
AC	014836				
DT	15-JUN-2002	(Rel. 41, Created)			
DT	15-JUN-2002	(Rel. 41, Last sequence update)			
DE	Tumor necrosis factor receptor superfamily member 13B (Transmembrane activator and CAML interactor).				
GN	TNFRSF13B OR TACI.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=B-cell;				
RX	MEDLINE=97458245; PubMed=9311921;				
RA	von Buelow G.-U., Bram R.U.;				
RT	"NF-AT activation induced by a CAML-interacting member of the tumor necrosis factor receptor superfamily.";				
RL	Science 278:138-141(1997).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Blood;				
RL	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RP	FUNCTION.				
RX	MEDLINE=20519647; PubMed=10956646;				
RA	Wu Y., Bressette D., Carrell J.A., Kaufman T., Peng P., Taylor K., Gan Y., Cho Y.H., Garcia A.D., Gollatz E., Dimke D., Lafleur D., Mlgone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J.,				
RA	Olgene H.S., Kanakara J. P., Moore P.A., Baker K.P.;				
RT	"Tumor necrosis factor (TNF) receptor superfamily member TACI is a high affinity receptor for TNF family members APRIL and BLys.";				
RL	J. Biol. Chem. 275:35478-35485 (2000).				
RN	[4]				
RP	FUNCTION.				
RX	MEDLINE=21170294; PubMed=10973284;				
RA	Yu G., Boone T., Delaney J., Hawkin N., Kelley M., Ramakrishnan M., McCabe S., Qiu W.R., Kormuc M., Xia X.-Z., Guo J., Scollina M., Boyle W.J., Sarosi I., Hsu H., Senaldi G., Thell L.E.;				
RT	"APRIL and TRAF-1 and receptors BCMA and TRAF1: system for regulating humoral immunity.";				
RL	Nat. Immunol. 1:252-256(2000).				
CC	-I- FUNCTION: Receptor for TNFSF13B/APRIL and TNFSF13B/TRAF1/BAFF/BLYS that binds both ligands with similar high affinity. Mediates calcineurin-dependent activation of NF-AT, as well as activation of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-cell function and the regulation of humoral immunity.				
CC	-I- SUBUNIT: Binds TRAF2, TRAF3 and TRAF6. Binds the NH2-terminal domain of CAML with its C-terminus.				
CC	-I- SUBCELLULAR LOCATION: Type III membrane protein.				
CC	-I- TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small intestine and peripheral blood leukocytes. Expressed in resting B-				

cells and activated T-cells, but not in resting T-cells.
 CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
 CC -1- CAUTION: It is uncertain whether Met-1 or Met-31 is the initiator.
 CC -----
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 CC -----
 CC EMBL: AF023614; AAC51790.1; -
 CC EMBL: BC028072; AAH28072.1; -
 CC GenBank: U00000; U00000.1; -
 CC MIM: 604907; -
 CC InterPro: IPR001368; TNFR_C6.
 CC PROSITE: PS00652; TNFR_NGFR_1; 1.
 CC PROSITE: PS00650; TNFR_NGFR_2; FALSE NEG.
 CC Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein;
 CC Repeat.
 CC DOMAIN 1 165 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 166 186 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 CC (POTENTIAL).
 CC REPEAT 187 293 CTOTOPLASTIC (POTENTIAL).
 CC REPEAT 33 67 TNFR-CYS 1.
 CC REPEAT 70 104 TNFR-CYS 2.
 CC DISULFID 34 47 BY SIMILARITY.
 CC DISULFID 50 62 BY SIMILARITY.
 CC DISULFID 54 66 BY SIMILARITY.
 CC DISULFID 71 86 BY SIMILARITY.
 CC DISULFID 89 100 BY SIMILARITY.
 CC DISULFID 93 104 BY SIMILARITY.
 CC CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CONFLICT 251 251 P -> L (TN REF. 2).
 CC SEQUENCE 293 AA, 31816 MW, 41179933DB17A5EB CRC64;
 CC
 CC Query Match 100.0%; Score 909; DB 1; Length 293;
 CC Best Local Similarity 100.0%; Pred. No. 4.3e-79;
 CC Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 MGLGSRGSRGSRVQDERPFGQMTGVAMSCPEEQYWDPLGTCMGCKTICNHSQR 60
 CC Db 1 MGLGSRGSRGSRVQDERPFGQMTGVAMSCPEEQYWDPLGTCMGCKTICNHSQR 60
 CC QY 61 TCAAFGRSISCRKQKFTDHLRDCISGASICGHPKCAVCEKLSPPVLPPELR 120
 CC Db 61 TCAAFGRSISCRKQKFTDHLRDCISGASICGHPKCAVCEKLSPPVLPPELR 120
 CC QY 121 QRSGEVENSNDNGRYQGLEHRSSEASPPALPGKLKADQVALVYST 166
 CC Db 121 QRSGEVENSNDNGRYQGLEHRSSEASPPALPGKLKADQVALVYST 166
 CC
 CC RESULT 2
 CC ID T13X MOUSE STANDARD; PRT; 249 AA.
 CC AC Q9ETB3; Q9DBZ3;
 CC DT 15-JUN-2002 (Rel. 41, Created)
 CC DT 15-JUN-2002 (Rel. 41, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
 CC activator and CAML interactor).
 CC GN TNFRSF13B OR TACI.
 CC OS Mus musculus (Mouse).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC Tissue= spleen;
 CC RX MEDLINE=21177254; PubMed=10881172;
 CC Yan M., Mörsters S.A., Grewal I.S., Wang H., Ashkenazi A.,

RA Dixit V.M.;
 RT "Identification of a receptor for Bvys demonstrates a crucial role in
 RT humoral immunity";
 RL Nat. Immunol. 1:37-41 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Komno H., Adachi J., Fukuda S.,
 RA Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yamazaki I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kanakawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bares G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guernicich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Saeki H., Sato K., Schoenbach C., Seye T., Shibata Y., Storch K.-P.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kontecki S.,
 RA Hayashizaki Y.;
 RL "Functional annotation of a full-length mouse cDNA collection";
 RN Nature 409:685-690 (2001).
 RP FUNCTION.
 RX MEDLINE=20341628; PubMed=10880535;
 RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
 RA Theill L.E., Colombero A., Solovjev I., Lee F., McCabe S., Elliott R.,
 RA Miner K., Hawkins J., Guo J., Stolina M., Yu G., Wang J., Delaney J.,
 RA Meng S.-Y., Boyle W.J., Heu H.;
 RT "TRAF1 is a TRAF-interacting receptor for TLR1-1, a tumor necrosis
 RT factor family member involved in B cell regulation";
 RL J. Exp. Med. 192:137-143 (2000).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=21322748; PubMed=11429548;
 RA Wang H., Mörsters S.A., Baker T., Chan B., Lee W.P., Fu L., Tumas D.,
 RA Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.;
 RT "TRAF1-ligand interactions are required for T cell activation and
 RT collagen-induced arthritis in mice";
 RL Nat. Immunol. 2:632-637 (2001).
 CC -1- FUNCTION: Receptor for TNFRSF13/APRIL and TNFRSF13B/BAFF/BLYS
 CC that binds both ligands with similar high affinity. Mediates
 CC calcineurin-dependent activation of NF-AT, as well as activation
 CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
 CC cell function and the regulation of humoral immunity (by
 CC similarity).
 CC -1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
 CC domain of CAML with its C-terminus (by similarity).
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein (probable).
 CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF257673; AAG0081.1; -
 CC EMBL: AK004668; BAB33457.1; -
 CC MGD: MGI:1889411; Tnftrsf13b.
 CC PROSITE: PS00652; TNFR_NGFR_1; 1.
 CC PROSITE: PS00650; TNFR_NGFR_2; 2.
 CC Receptor; Immune response; Signal-anchor; Transmembrane; Repeat.
 CC DOMAIN 1 128 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 129 149 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)

FT DOMAIN 150 249 (POTENTIAL).
 FT REPEAT 5 38 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 42 76 TNFR-CYS 1.
 FT DISULFID 6 19 BY SIMILARITY.
 FT DISULFID 22 34 BY SIMILARITY.
 FT DISULFID 26 38 BY SIMILARITY.
 FT DISULFID 43 58 BY SIMILARITY.
 FT DISULFID 61 72 BY SIMILARITY.
 FT DISULFID 65 76 BY SIMILARITY.
 FT CONFLICT 137 I -> F (IN REF. 2).
 SQ SEQUENCE 249 AA; 26947 MM; CBF2D61C2931D81 CXC64;
 Query Match 46.1%; Score 419.5; DB 1; Length 249;
 Best Local Similarity 55.1%; Pred. No. 8.6e-33;
 Matches 76; Conservative 22; Mismatches 31; Indels 9; Gaps 2;

Qy 29 VAMRCEBQYVDPILGTCMSCKTICNHSQRTCAAFCSLSCKRQKFTYHLRDCIS 88
 Db 1 MAMAPCPDQYWDSSRKSCVSCALTCQSGRQRTCTDPCFKFICRKEQGRYDHLGACVS 60
 Qy 89 CASIOGHPKOCACFCENKLRSPVNLPELRRQBSGEVNNSDNGRGYQGLEHRSSEASP 148
 Db 61 CDSTGTHPQOCAPHCRCRPSQANLQPELGRPOAGEVEVRSDNGRQSGSHG----- 114
 Qy 149 ALPGIKLSADQVALVYST 166
 Db 115 --PGLRLSSDQLT-YCT 129

RESULT 3
 ID PKCS MOUSE STANDARD; PRT; 1877 AA.
 AC 004592; 062040;
 DT 01-FEB-1995 (Rel. #1, Created)
 DT 16-OCT-2001 (Rel. #0, Last sequence update)
 DT 15-JUN-2002 (Rel. #1, Last annotation update)
 DB PROTEIN CONVERTASE SUBTILISIN/KEXIN TYPE 5 PRECURSOR (EC 3.4.21.-)
 DB (Protein convertase PCS5) (Subtilisin/kexin-like protease PCS5)
 DB (Convertase PCS5) (PC6) (Subtilisin-like proprotein convertase 6) (SEPC6).
 DE PCSK5.
 GN PCSK5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 330-1877 FROM N.A. (ISOFORM PCSB).
 RC STRAIN=ICR; TISSUE=Intestine;
 RA MEDLINE=93327934; PubMed=8335106;
 RA Nakagawa T., Murakami K., Nakayama K.;
 RT "Identification of an isoform with an extremely large Cys-rich region
 of PC6, a Kex2-like processing endoprotease.";
 RL FEBS Lett. 327:165-171 (1993).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM PCSA).
 RC TISSUE=Brain, and Intestine;
 RA MEDLINE=93224489; PubMed=8468318;
 RA Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K.,
 RA Nakayama K.;
 RT "Identification and functional expression of a new member of the
 mammalian Kex2-like processing endoprotease family: its striking
 structural similarity to PACB4.";
 RL J. Biochem. 113:132-135 (1993).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM PCSA).
 RC TISSUE=Adrenal cortex;
 RA MEDLINE=93342056; PubMed=8341687;
 RA Ianson J., Vleau D., Hamelin J., Day R., Chretien M., Seidah N.G.;
 RT "cDNA structure of the mouse and rat subtilisin/kexin-like PCS5: a
 candidate proprotein convertase expressed in endocrine and
 nonendocrine cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695 (1993).

RN [4]
 RP PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION.
 RX MEDLINE=97103178; PubMed=8947550;
 RA De Bie I., Marcinkiewicz M., Malide D., Lazure C., Nakayama K.,
 RA Bandayan M., Seidah N.G.;
 RT "The isoforms of proprotein convertase PCS are sorted to different
 subcellular compartments.";
 RL J. Cell Biol. 135:1261-1275 (1996).
 RN [5]
 RP DEVELOPMENTAL EXPRESSION.
 RX MEDLINE=96293359; PubMed=8698813;
 RA Constam D.B., Calton M., Robertson E.J.;
 RT "SPC4, SPC6, and the novel protease SPC7 are coexpressed with bone
 morphogenetic proteins at distinct sites during embryogenesis.";
 RL J. Cell Biol. 134:181-191 (1996).
 RN [6]
 RP DEVELOPMENTAL EXPRESSION.
 RX MEDLINE=97436919; PubMed=9291583;
 RA Rancourt S.L., Rancourt D.E.;
 RT "Murine subtilisin-like proteinase SPC6 is expressed during embryonic
 implantation, somitogenesis, and skeletal formation.";
 RL Dev. Genet. 21:75-81 (1997).
 CC -1- FUNCTION: LIKELY TO REPRESENT A WIDESPREAD ENDOPEPTASE ACTIVITY
 WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE
 OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF. MAY BE RESPONSIBLE
 FOR THE MATURATION OF GASTROINTESTINAL PEPTIDES. MAY BE INVOLVED
 IN THE CELLULAR PROLIFERATION OF ADRENAL CORTEX VIA THE ACTIVATION
 OF GROWTH FACTORS.
 CC -1- CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR
 PROTEININS BY CLEAVAGE OF ARG-XAA-YAA-ARG-|-ZAA BONDS, WHERE XAA
 CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
 CC -1- SUBCELLULAR LOCATION: PCSA IS SECRETED THROUGH THE REGULATED
 SECRETORY PATHWAY. PCSB IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO
 A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH
 EARLY ENDOSOMES.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS, PCSB/LONG (SHOWN HERE)
 AND PCSA/SHORT; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: PCSA IS EXPRESSED IN MOST TISSUES BUT IS MOST
 ABUNDANT IN THE INTESTINE AND ADRENALS. PCSB IS EXPRESSED IN THE
 INTESTINE, ADRENALS AND LUNG BUT NOT IN THE BRAIN.
 CC -1- DEVELOPMENTAL STAGE: WEAKLY EXPRESSED THROUGHOUT THE EMBRYO,
 EXCEPT IN THE DEVELOPING NERVOUS SYSTEM, THE RIBS AND THE LIVER,
 BUT MARKEDLY UPREGULATED AT DISCRETE SITES DURING DEVELOPMENT. AT
 E6.5, PROMINENT EXPRESSION OBSERVED IN DIFFERENTIATED DECIDUA. AT
 E7.5, INTENSE EXPRESSION IN EXTRAEMBRYONIC ENDODERM, ANION AND
 NASCENT MESODERM. AT 8.5, ABUNDANT EXPRESSION IN SOMITES AND YOLK
 SAC FOLLOWED BY A CONTINUATION TO DERMATOME COMPARTMENT. BETWEEN
 E9.5 AND E11.5, ABUNDANT EXPRESSION IN AER (THICKENED ECTODERMAL
 CELLS OF LIMB BUDS). AT E12.5, EXPRESSION IN THE LIMBS IS CONFINED
 TO THE CONDENSING MESenchym SURROUNDING THE CARILAGE. AT THIS
 STAGE, STRONG EXPRESSION ALSO DETECTED IN VERTEBRAL AND FACIAL
 CARILAGE PRIMORDIA AND IN THE MUSCLE OF THE TONGUE. AT E16.5,
 CC ABUNDANT EXPRESSION IN EPITHELIAL CELLS OF THE INTESTINAL VILLI.
 CC ISOFORM A IS MOST ABUNDANT AT ALL STAGES BUT SIGNIFICANT LEVELS OF
 ISOFORM B OCCUR AT E12.5.
 CC -1- DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
 ASSISTING THE FOLDING OF THE ZMOGEN WITHIN THE ENDOPLASMIC
 RETICULUM.
 CC -1- DOMAIN: AC 1 AND AC 2 (CLUSTERS OF ACIDIC AMINO ACIDS) CONTRAIN
 SORTING INFORMATION. AC 1 DIRECTS TEN LOCALIZATION AND INTERACTS
 WITH THE TGN SORTING PROTEIN PACS-1.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
 CC -1- SIMILARITY: CONTAINS 1 HOWO B/P DOMAIN.
 CC -----
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 CC -----
 DR EMBL; D17583; BAA04507.1; -.

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DR EMBL: D12619; BAA02143.1; -.
DR EMBL: L14932; AAA74636.1; -.
DR PIR: JX0248; JX0248.
DR PIR: A48225; A48225.
DR HSSP: 099405; IMPR.
DR MEROPS: S08_076; -.
DR MGD: MGI:97515; Pck5.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR002174; Furin-like.
DR InterPro: IPR002884; P_domain.
DR InterPro: IPR000209; Peptidase_S8.
DR Pfam: PR00082; Peptidase_S8; 1.
DR Pfam: PF01483; P; PARTIAL.
DR PRINTS: PR00723; SUBTILISIN.
DR ProDom: PD000717; P_domain; 1.
DR SMART: SM00001; EGF_1like; 2.
DR SMART: SM00261; FU_22.
DR PROSITE: PS00136; SUBTILASE_ASP; 1.
DR PROSITE: PS00137; SUBTILASE_HIS; 1.
DR PROSITE: PS00138; SUBTILASE_SER; 1.
DR Hydrolase: Serine protease; Zymogen; Signal;
KM Cleavage on pair of basic residues; Repeat; Alternative splicing;
KW Transmembrane.
FT SIGNAL 1 34
FT PROPEP 35 116
FT CHAIN 117 1877
FT DOMAIN 117 1768 PROTEIN CONVERTASE SUBTILISIN/KEXIN
FT TRASMEN 1769 1789 TYPE 5.
FT DOMAIN 1790 1877 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 117 452 POTENTIAL.
FT DOMAIN 464 602 CTOPOLASMIC (POTENTIAL).
FT DOMAIN 638 1753 CATALYTIC.
FT DOMAIN 1825 1844 HOMO B.
FT DOMAIN 1856 1877 CYS-RICH MOTIF (CRM) REGION.
FT SITE 116 117 AC 1.
FT SITE 521 523 AC 2.
FT ACT_SITE 173 523 CLEAVAGE (AUTO-) (BY SIMILARITY).
FT ACT_SITE 214 214 CELL ATTACHMENT SITE (POTENTIAL).
FT ACT_SITE 388 388 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 227 227 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CARBOHYD 383 383 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 667 667 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 754 754 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 804 804 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 854 854 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 951 951 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1016 1016 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1220 1220 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1317 1317 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1523 1523 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1711 1711 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1733 1733 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARSPLIC 878 915 GEYIDQGHCTCEASCKAKPTEDCISCVTVLD ->
FT VARSPLIC 916 1877 ATEESWAEAGFMTLVKKNLCQKRVLDQCCCTCTFOG
FT VARSPLIC 1877 1877 MISSING (IN ISOFORM PCSA).
SQ SEQUENCE 1877 AA; 209287 MW; EC850E2DF20EALIC3 CRC64;

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Query Match 10.7%; Score 97.5; DB 1; Length 1877;
 Best Local Similarity 30.2%; Pred. No. 0.21;
 Matches 29; Conservative 12; Mismatches 32; Indels 23; Gaps 7;

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QY 14 RYDQ--EEEPFGQIMTVGAMRSGPREQYWDPLG-TCMSCKITCN-----HQSQRCAAF 65
DB 956 RADKIGQGEF---LYHGECLNCPVGHY--PAKGHTCLCPDPNCELCTPNPHICSRMSGY 1010
QY 66 -----CRSLCKRKGQKPYDHLRLDCTSCASIC 93
DB 1011 VIIPNHTQCKLECR--QGEFQDSFEYECMPCBEGC 1044

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RESULT 4
ID Y2A CAEBL STANDARD; PRT; 867 AA.
AC P34447; P34448;
DT 01-FEB-1994 (Rel. 28, Created)
DT 15-UN-2002 (Rel. 41, Last sequence update)
DT 15-UN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein F54F2.2 in chromosome III, isoform a.
GN F54F2.2/F54F2.3/F54F2.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OK NCBI_taxid=6239;
RP [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Br1stol N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ahncough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kerhaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Sims M., Smaildon N., Smith A., Smith M., Sonnenhammer B., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Woldman P.;
RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RT Nature 368:32-38(1994).
RL [2]
RP REVISIONS, AND ALTERNATIVE SPLICING.
RA Waterson R.;
RE Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; a (shown here) and b (AC
CC P34448); may be produced by alternative splicing.
CC -1- SIMILARITY: CONTAINS 2 PHD ZINC-FINGER DOMAINS.
-----
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CC EMBL: U23645; AAK26137.1; -.
DR PIR: S44827; S44827.
DR WormPep: F54F2.2a; CE25003.
DR InterPro: IPR001965; Znf_PHD.
DR Pfam: PR00628; PHD; 1.
DR SMART: SM00249; PHD; 2.
KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger; Repeat;
KW DNA-binding; Nuclear protein; Alternative splicing.
FT ZN_FING 5 57 PHD-TYPE 1.
FT ZN_FING 124 185 PHD-TYPE 2.
SQ SEQUENCE 867 AA; 92189 MW; 7B582DC2529CFEAD CRC64;

```

Query Match 9.8%; Score 89; DB 1; Length 867;
 Best Local Similarity 32.5%; Pred. No. 0.61;
 Matches 27; Conservative 8; Mismatches 28; Indels 20; Gaps 5;

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QY 34 CPREQYWPPLIGTQSC-KTICNHSORTCAFCRLSCREQKPYDHLRLDCTSCASI 92
DB 130 CNEEPFNPAKKGACMSCKSTCKSFHYTCAQ-RKGLLC--EEGAI----- 172
QY 93 CGQHPKQCAVFCENTLRQVNL 115
DB 173 -SRNVKTCGY-CENHLKRAINDP 193

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RESULT 5		PRT: 297 AA.	
ID	XEDA HUMAN	STANDARD:	
AC	Q9HAV5;		
DT	15-JUN-2002 (Rel. 41, Created)		
DT	15-JUN-2002 (Rel. 41, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Tumor necrosis factor receptor superfamily member XEDAR (X-linked ectodysplasin-A2 receptor) (EDA-A2 receptor).		
GN	XEDAR.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A., AND MUTAGENESIS OF GLU-256.		
RC	TISSUE=Fetal kidney;		
RX	Medline=20495245; PubMed=11039935;		
RA	Yan M., Wang L.-C., Hymowitz S.G., Schildbach S., Lee J., Goddard A., de Vos A.M., Gao W.-Q., Dixit V.M.;		
RT	"Two-amino acid molecular switch in an epithelial morphogen that regulates binding to two distinct receptors.";		
RL	Science 290:523-527(2000).		
CC	-I- FUNCTION: Receptor for EDA isoform A2, but not for EDA isoform A1. Mediates the activation of NF-kappa-B. Activation seems to be mediated by binding to TRAF6.		
CC	-I- SUBUNIT: Associates with TRAF1, TRAF3 and TRAF6.		
CC	-I- SUBCELLULAR LOCATION: Type III membrane protein.		
CC	-I- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.		
CC	-----		
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CC	-----		
DR	EMBL; AF298812; AAG28761.1; -		
DR	MIM; 300276; -		
DR	InterPro; IPR001368; TNFR_C6.		
DR	Pfam; PR00020; TNFR_C6; 2.		
DR	SMART; SM00208; TNFR; 2.		
DR	PROSITE; PS00652; TNFR_NGFR_1; 2.		
DR	PROSITE; PS0050; TNFR_NGFR_2; 2.		
KW	Receptor; Developmental protein; Differentiation; Transmembrane; Glycoprotein; Repeat.		
KW	DOMAIN	1	138
FT	TRANSMEM	139	159
FT			
FT	DOMAIN	160	297
FT	REPEAT	2	41
FT	REPEAT	43	83
FT	REPEAT	85	118
FT	DISULFID	3	15
FT	DISULFID	18	31
FT	DISULFID	21	41
FT	DISULFID	44	58
FT	DISULFID	61	75
FT	DISULFID	64	83
FT	DISULFID	86	104
FT	DISULFID	107	118
FT	CARBOHYD	74	74
FT	MUTAGEN	256	256
FT	SEQUENCE	297 AA;	32728 MM;
QY	Query Match	9.5%;	Score 86; DB 1; Length 297;
	Best Local Similarity	22.0%;	Pred. No. 0.4;
	Matches 26; Conservative	19;	Mismatches 31; Indels 42; Gaps 7;
DB	3	COENZYME-DB	WDRYQVTCOR-CGPGGGLSDCGGEGGDYVCTACPRRYKSSWGHHRCDS 60

DB	61	CITCAVINRQKAKVNTATSNACGD	-----C-----	LPFRFKRRIRIGLQD	101
Oy	86	CISC	-----SICQHPROCAVFPENKLSRSPVNIPELRARSRSEVEN	128	
Db	61	CITCAVINRQKAKVNTATSNACGD	-----C-----	LPFRFKRRIRIGLQD	101
RESULT 6					
RECK_MOUSE					
ID	RECK_MOUSE	STANDARD;	PRT;	971 AA.	
AC	O92011				
DT	15-JUN-2002	(Rel. 41, Created)			
DT	15-JUN-2002	(Rel. 41, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Reversion-inducing cysteine-rich protein with Kazal motifs precursor (mRECK).				
GN	RECK.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.				
OX	NCBI_TaxID=10090;				
RA	[1]				
RA	SEQUENCE FROM N.A.				
RL	MEDLINE=99007295; PubMed=9789069;				
CC	Kitayama H., Sheng Z., Horan T.P., Kitayama H., Maki M., Hltomi K.,				
CC	Kitayama Y., Takai S., Sasahara R.M., Horimoto A., Ikawa Y.,				
CC	Ratzkin B.J., Arakawa T., Noda M.;				
CC	"Regulation of matrix metalloproteinase-9 and inhibition of tumor				
CC	invasion by the membrane-anchored glycoprotein RECK.";				
CC	Proc. Natl. Acad. Sci. U.S.A. 95:13221-13226(1998).				
CC	-1- FUNCTION: Negatively regulates matrix metalloproteinase-9 (MMP-9)				
CC	by suppressing MMP-9 secretion, and by direct inhibition of its				
CC	enzymatic activity. RECK down-regulation by oncogenic signals may				
CC	facilitate tumor invasion and metastasis. Appears to also				
CC	regulate MMP-2 and MT1-MMP, which are involved in cancer				
CC	progression (By similarity).				
CC	-1- SUBUNIT: Interacts with MMP-9.				
CC	-1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.				
CC	-1- DEVELOPMENTAL STAGE: In E10.5 embryos the RECK protein is widely				
CC	expressed in mesenchymal tissues and is relatively abundant in the				
CC	marginal zone of the neural tube and large blood vessels such as				
CC	the aorta.				
CC	-1- SIMILARITY: CONTAINS 3 KAZAL-LIKE DOMAINS.				
CC	-----				
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CC	or send an email to license@sib-sib.ch).				
CC	-----				
DR	EMBL; AB006960; BAA34061.1; -				
DR	MED; MG1:1855698; RECK.				
DR	InterPro; IPR002350; Kazal.				
DR	Pfam; PF00050; Kazal; 2.				
DR	SMART; PS00280; KAZAL; 2.				
DR	PROSITE; PS00282; KAZAL; 1.				
KW	Signal; Glycoprotein; GPI-anchor; Serine protease inhibitor;				
KW	Membrane; Anti-oncogene; Repeat.				
FT	SIGNAL	1	22		
FT	CHAIN	23	942		
FT					
FT	PROPEP	943	971		
FT	LIPID	942	942		
FT	DOMAIN	633	677		
FT	DOMAIN	704	750		
FT	DOMAIN	751	787		
FT	DOMAIN	37	338		
FT	REPEAT	37	84		
FT	REPEAT	104	141		
FT	REPEAT	151	197		
FT	REPEAT	216	263		
FT	REPEAT	292	338		
FT					

```

FT DISULFID 635 654 BY SIMILARITY.
FT DISULFID 633 658 BY SIMILARITY.
FT DISULFID 677 677 BY SIMILARITY.
FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 971 AA; 106134 MW; 2FC8BEB38A20F86D CRC64;

Query Match 9.1%; Score 83; DB 1; Length 971;
Best Local Similarity 22.4%; Pred. No. 2.5;
Matches 33; Conservative 16; Mismatches 42; Indels 56; Gaps 8;

QY 34 CPEE-QYMDPL-----LGTG-----MSCRTICNHQSORTCAFCRSLS 70
DB 74 CPETWEIWSNMSNSLPVFKSKDGMVGGCCGLAIGLEGRQACQKASKNDI----SKY 129
QY 71 CRKQCKFIDHLRDCIS-----CASTCGQHPKOCANFCENKLRSPVNLPELRRORS 123
DB 130 CRKE-----YENALFSCISRNEMGSVCCSYAGHH-TWCRFCQAFRT----- 171
QY 124 GEVENSDNSGRYQGLEHGRSEASPAL 150
DB 172 ----DSSPGSPQIKAVENYCASTISPOL 194

RESULT 7
APMU_PIG STANDARD; PRT; 1150 AA.
AC P12021;
DT 01-OCT-1989 (rel. 12, Created)
DT 01-DEC-1992 (rel. 24, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Apomucin (Mucin core protein) (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP TISSUE=Submaxillary gland;
RC MEDLINE=91236743; PubMed=2033060;
RA Eckhardt A.E., Timpte C.S., Abernethy J.L., Zhao Y., Hill R.L.;
RT "Porcine submaxillary mucin contains a cysteine-rich,
RT carboxyl-terminal domain in addition to a highly repetitive,
RT glycosylated domain.";
RL J. Biol. Chem. 266:9678-9686(1991).
RN [2]
RP TISSUE=Submaxillary gland;
RC MEDLINE=88087170; PubMed=2826455;
RA Timpte C.S., Eckhardt A.E., Abernethy J.L., Hill R.L.;
RT "Porcine submaxillary gland apomucin contains tandemly repeated,
RT identical sequences of 81 residues.";
RL J. Biol. Chem. 263:1081-1088(1988).
RN [3]
RP TISSUE=Submaxillary gland;
RC MEDLINE=87280230; PubMed=3611111;
RA Eckhardt A.E., Timpte C.S., Abernethy J.L., Toumadje A.,
RA Johnson W.C. Jr., Hill R.L.;
RT "Structural properties of porcine submaxillary gland apomucin.";
RL J. Biol. Chem. 262:11339-11344(1987).
RN [4]
RP CARBOHYDRATE-LINKAGE SITES, AND SEQUENCE OF 45-125.
RC TISSUE=Submaxillary gland;
RX MEDLINE=97248516; PubMed=9092502;
RA Gerken T.A., Owens C.L., Pasumathy M.;
RT "Determination of the site-specific O-glycosylation pattern of the
RT porcine submaxillary mucin tandem repeat glycopeptide. Model proposed
RT for the polypeptide:galnac transferase peptide binding site.";
RL J. Biol. Chem. 272:9709-9719(1997).

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CC -1 FUNCTION: APOMUCIN IS PART OF MUCIN, THE MAJOR GLYCOPROTEIN
CC SYNTHESIZED AND SECRETED BY MUCOUS CELLS OF THE SUBMAXILLARY
CC GLAND. ITS HIGHLY VISCOUS AQUEOUS SOLUTIONS SERVE TO LUBRICATE
CC THE ORAL CAVITY AND TO PROTECT IT FROM THE EXTERNAL
CC ENVIRONMENT.
CC -1 SUBUNIT: INTERMOLECULAR DISULFIDE BONDS COULD HELP MAINTAIN A
CC MULTIMERIC MUCIN STRUCTURE.
CC -1 SUBCELLULAR LOCATION: Secreted.
CC -1 TISSUE SPECIFICITY: SUBMAXILLARY MUCOSAE.
CC -1 DOMAIN: CONTAINS TANDEMLY REPEATED, IDENTICAL SEQUENCES OF 81
CC RESIDUES.
CC -1 PTM: EXTENSIVELY O-LINKED GLYCOSYLATED ON SER AND THR RESIDUES OF
CC THE REPEAT UNITS. HIGHEST GLYCOSYLATION APPEARS TO OCCUR ON SER
CC RESIDUES WHICH HAVE GLY AT POSITIONS AT +2 OR -2 FROM THE
CC GLYCOSYLATION SITE OR, WHERE GLY IS THE PENULTIMATE RESIDUE, THE
CC PRESENCE OF PROLINE (USUALLY AT POSITION +3 OR -3) APPEARS TO ALSO
CC ENHANCE GLYCOSYLATION.
CC -1 SIMILARITY: CONTAINS 1 WFRC DOMAIN.
CC -1 SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE (CTCK) DOMAIN.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements/
CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; M61883; AAA30998.1; -.
CC EMBL; M21174; AAA30990.1; -.
CC PIR; A40009; A40009.
CC InterPro; IPR000359; Cys_knot.
CC InterPro; IPR01007; WFRC.
CC Pfam; PF00007; Cys_knot; 1.
CC SMART; SM00041; CT_1.
CC SMART; SM00214; WMC_1.
CC PROSITE; PS01185; CTCK_1, 1.
CC PROSITE; PS01225; WFRC_2, 1.
CC PROSITE; PS01208; WFC; 1.
CC DR Glycoprotein; Repeat.
CC KM NON TER 1 368 81 AA TANDEM REPEATS.
CC FT DOMAIN <1 44 1.
CC FT REPEAT 45 125 2.
CC FT REPEAT 126 206 3.
CC FT REPEAT 207 287 4.
CC FT REPEAT 288 368 5.
CC FT REPEAT 369 391 6 (INCOMPLETE).
CC FT DOMAIN 929 995 WFC.
CC FT DOMAIN 1062 1146 CTCK.
CC FT DISULFID 1062 1109 BY SIMILARITY.
CC FT DISULFID 1076 1123 BY SIMILARITY.
CC FT DISULFID 1085 1139 BY SIMILARITY.
CC FT DISULFID 1089 1141 BY SIMILARITY.
CC FT DISULFID ? 1145 BY SIMILARITY.
CC FT CARBOHYD 46 46 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 50 50 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 51 51 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 57 57 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 58 58 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 61 61 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 66 66 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 67 67 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 73 73 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 74 74 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 76 76 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 77 77 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 81 81 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 83 83 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 87 87 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 91 91 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 93 93 O-LINKED (GALNAC. . .) (MUCIN TYPE).
CC FT CARBOHYD 94 94 O-LINKED (GALNAC. . .) (MUCIN TYPE).

```


Db 772 --EDGRYFNG--ODCPCRFECATCAGAGADGCTGEGYFEMD 811

RESULT 9

LRP2_RAT

ID_LRP2_RAT STANDARD; PRT; 4660 AA.

AC P98158; 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Low-density lipoprotein receptor-related protein 2 precursor (Megalyn)

DE (Glycoprotein 330).

GN LRP2.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Kidney;

RX MEDLINE=95024033; PubMed=7937880;

RA Saito A., Piemromaco S., Loo A.K.C., Farquhar M.G.;

RT "Complete cloning and sequencing of rat gp330/'megalyn,' a

RT distinctive member of the low density lipoprotein receptor gene

RT family.";

RL Proc. Natl. Acad. Sci. U.S.A. 91:9725-9729(1994).

RL [2]

RP FUNCTION.

RX MEDLINE=95386696; PubMed=7544804;

RA Moestrup S.K., Cui S., Vorum H., Bregengaard C., Bjorn S.E.,

RA Norris K., Gilemann U., Christensen E.I.;

RT "Evidence that epithelial glycoprotein 330/megalyn mediates uptake of

RT polybasic drugs.";

RL J. Clin. Invest. 96:1404-1413(1995).

RN [3]

RP TISSUE SPECIFICITY.

RX MEDLINE=94172242; PubMed=7510321;

RA Zheng G., Bachlueky D.R., Stamenkovic I., Strickland D.K., Brown D.,

RA Andres G., McCluskey R.T.;

RT "Organ distribution in rats of two members of the low-density

RT lipoprotein receptor gene family, gp330 and LRP/alpha 2MR, and the

RT receptor-associated protein (RAP).";

RL J. Biochem. 121:531-542(1994).

CC -1- FUNCTION: BINDS PLASMINOGEN, EXTRACELLULAR MATRIX COMPONENTS,

CC PLASMINOGEN ACTIVATOR-PLASMINOGEN ACTIVATOR INHIBITOR TYPE I

CC COMPLEX, APOLOPROTEIN B-ENRICHED BETA-VLDL, LIPOPROTEIN LIPASE,

CC LACTOFERRIN, CLUSTERIN AND CALCIUM.

CC -1- FUNCTION: RECEPTOR-MEDIATED UPTAKE OF POLYBASIC DRUGS SUCH AS

CC APROUTININ, AMINOGLYCOSIDES AND POLYMYXIN B.

CC -1- SUBUNIT: FORMS A MULTIMERIC COMPLEX TOGETHER WITH A RECEPTOR-

CC ASSOCIATED PROTEIN (RAP).

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXPRESSED IN

CC CLATHRIN-COATED PITS; A SOLUBLE FORM IS POSSIBLY DERIVED BY

CC CLEAVAGE AT THE CELL SURFACE.

CC -1- TISSUE SPECIFICITY: EPITHELIAL CELLS OF KIDNEY GLOMERULUS AND

CC PROXIMAL TUBULE, LUNG, EPIDIDYMIS, YOLK SAC, AMONG OTHERS.

CC -1- SIMILARITY: CONTAINS 36 LDL-RECEPTOR CLASS A DOMAINS.

CC -1- SIMILARITY: CONTAINS 37 LDL-RECEPTOR CLASS B DOMAINS.

CC -1- SIMILARITY: CONTAINS 17 EGF-LIKE DOMAINS.

CC -----

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; L34049; AAA5369.1; -.

DR HSSP; 007954; 1CR8.

DR GlycoSiteDB; P98158; -.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR001881; EGF-Ca.

DR InterPro; IPR002172; LDL_recept_A.

DR InterPro; IPR000033; ldl_receptor_rep.

DR Pfam; PF00057; ldl_recept_a; 36.

DR Pfam; PF00059; ldl_recept_b; 33.

DR PRINTS; PR00261; LDLRECEPTOR.

DR SMART; SM00179; EGF_CA; 3.

DR SMART; SM00001; EGF_Like; 15.

DR SMART; SM00192; LDLA; 36.

DR SMART; SM00135; LY; 35.

DR PROSITE; PS00010; ASX_HYDROXYL; 4.

DR PROSITE; PS00022; EGF_1; 1.

DR PROSITE; PS01186; EGF_2; 8.

DR PROSITE; PS01187; EGF_CA; 3.

DR PROSITE; PS01209; LDLRA_1; 31.

DR PROSITE; PS00068; LDLRA_2; 36.

KW Glycoprotein; Repeat; Endocytosis; Coated pits; Transmembrane;

KW Receptor; EGF-like domain; SH3-binding; Signal.

FT SIGNAL 1 25

FT CHAIN 1 4660

FT

FT DOMAIN 26 4425

FT TRANSMEM 4426 4446

FT 4447 4660

FT DOMAIN 26 64

FT 65 105

FT DOMAIN 106 144

FT 145 181

FT DOMAIN 181 219

FT 220 258

FT DOMAIN 263 307

FT 308 346

FT DOMAIN 347 385

FT 386 435

FT DOMAIN 435 476

FT 476 519

FT DOMAIN 521 566

FT 567 611

FT DOMAIN 612 652

FT 653 704

FT DOMAIN 704 752

FT 753 793

FT DOMAIN 793 835

FT 836 879

FT DOMAIN 881 923

FT 924 969

FT DOMAIN 969 1023

FT 1024 1103

FT DOMAIN 1103 1146

FT 1147 1186

FT DOMAIN 1186 1225

FT 1226 1269

FT 1270 1308

FT DOMAIN 1311 1351

FT 1352 1390

FT DOMAIN 1391 1430

FT 1431 1479

FT DOMAIN 1479 1523

FT 1524 1563

FT 1564 1609

FT DOMAIN 1611 1654

FT 1655 1696

FT DOMAIN 1697 1742

FT 1743 1791

FT DOMAIN 1791 1832

FT 1833 1882

FT DOMAIN 1883 1930

FT 1931 1972

FT DOMAIN 1973 2013

FT 2014 2060

FT DOMAIN 2061 2108

FT 2109 2156

FT DOMAIN 2157 2201

FT 2202 2245

FT DOMAIN 2246 2289

FT 2290 2332

FT DOMAIN 2333 2384

FT 2385 2433

FT DOMAIN 2434 2477

FT

FT LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED

FT PROTEIN 2.

FT EXTRACELLULAR (POTENTIAL).

FT POTENTIAL.

FT CYTOPLASMIC (POTENTIAL).

FT LDL-RECEPTOR CLASS A 1.

FT LDL-RECEPTOR CLASS A 2.

FT LDL-RECEPTOR CLASS A 3.

FT LDL-RECEPTOR CLASS A 4.

FT LDL-RECEPTOR CLASS A 5.

FT LDL-RECEPTOR CLASS A 6.

FT LDL-RECEPTOR CLASS A 7.

FT EGF-Like 1.

FT EGF-Like 2.

FT LDL-RECEPTOR CLASS B 1.

FT LDL-RECEPTOR CLASS B 2.

FT LDL-RECEPTOR CLASS B 3.

FT LDL-RECEPTOR CLASS B 4.

FT LDL-RECEPTOR CLASS B 5.

FT EGF-Like 3.

FT LDL-RECEPTOR CLASS B 6.

FT LDL-RECEPTOR CLASS B 7.

FT LDL-RECEPTOR CLASS B 8.

FT LDL-RECEPTOR CLASS B 9.

FT EGF-Like 4.

FT LDL-RECEPTOR CLASS A 8.

FT LDL-RECEPTOR CLASS A 9.

FT LDL-RECEPTOR CLASS A 10.

FT LDL-RECEPTOR CLASS A 11.

FT LDL-RECEPTOR CLASS A 12.

FT LDL-RECEPTOR CLASS A 13.

FT LDL-RECEPTOR CLASS A 14.

FT LDL-RECEPTOR CLASS A 15.

FT EGF-Like 5.

FT EGF-Like 6.

FT LDL-RECEPTOR CLASS B 10.

FT LDL-RECEPTOR CLASS B 11.

FT LDL-RECEPTOR CLASS B 12.

FT LDL-RECEPTOR CLASS B 13.

FT LDL-RECEPTOR CLASS B 14.

FT EGF-Like 7.

FT LDL-RECEPTOR CLASS B 15.

FT LDL-RECEPTOR CLASS B 16.

FT LDL-RECEPTOR CLASS B 17.

FT LDL-RECEPTOR CLASS B 18.

FT LDL-RECEPTOR CLASS B 19.

FT EGF-Like 8.

FT LDL-RECEPTOR CLASS B 20.

FT LDL-RECEPTOR CLASS B 21.

FT LDL-RECEPTOR CLASS B 22.

FT LDL-RECEPTOR CLASS B 23.

FT LDL-RECEPTOR CLASS B 24.

FT EGF-Like 9.

FT LDL-RECEPTOR CLASS B 25.

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FT DOMAIN 2479 2518 LDL-RECEPTOR CLASS B 26.
FT DOMAIN 2520 2562 LDL-RECEPTOR CLASS B 27.
FT DOMAIN 2564 2604 LDL-RECEPTOR CLASS B 28.
FT DOMAIN 2605 2647 LDL-RECEPTOR CLASS B 29.
FT DOMAIN 2652 2694 EGF-LIKE 10.
FT DOMAIN 2699 2739 LDL-RECEPTOR CLASS A 16.
FT DOMAIN 2740 2778 LDL-RECEPTOR CLASS A 17.
FT DOMAIN 2779 2820 LDL-RECEPTOR CLASS A 18.
FT DOMAIN 2821 2862 LDL-RECEPTOR CLASS A 19.
FT DOMAIN 2863 2903 LDL-RECEPTOR CLASS A 20.
FT DOMAIN 2906 2947 LDL-RECEPTOR CLASS A 21.
FT DOMAIN 2948 2992 LDL-RECEPTOR CLASS A 22.
FT DOMAIN 2993 3031 LDL-RECEPTOR CLASS A 23.
FT DOMAIN 3032 3072 LDL-RECEPTOR CLASS A 24.
FT DOMAIN 3075 3112 LDL-RECEPTOR CLASS A 25.
FT DOMAIN 3113 3153 EGF-LIKE 11.
FT DOMAIN 3154 3194 EGF-LIKE 12.
FT DOMAIN 3241 3282 LDL-RECEPTOR CLASS B 30.
FT DOMAIN 3284 3333 LDL-RECEPTOR CLASS B 31.
FT DOMAIN 3335 3377 LDL-RECEPTOR CLASS B 32.
FT DOMAIN 3379 3420 LDL-RECEPTOR CLASS B 33.
FT DOMAIN 3421 3461 LDL-RECEPTOR CLASS B 34.
FT DOMAIN 3467 3511 EGF-LIKE 13.
FT DOMAIN 3512 3552 LDL-RECEPTOR CLASS A 26.
FT DOMAIN 3553 3593 LDL-RECEPTOR CLASS A 27.
FT DOMAIN 3594 3634 LDL-RECEPTOR CLASS A 28.
FT DOMAIN 3635 3675 LDL-RECEPTOR CLASS A 29.
FT DOMAIN 3678 3718 LDL-RECEPTOR CLASS A 30.
FT DOMAIN 3719 3759 LDL-RECEPTOR CLASS A 31.
FT DOMAIN 3759 3797 LDL-RECEPTOR CLASS A 32.
FT DOMAIN 3798 3836 LDL-RECEPTOR CLASS A 33.
FT DOMAIN 3842 3882 LDL-RECEPTOR CLASS A 34.
FT DOMAIN 3883 3924 LDL-RECEPTOR CLASS A 35.
FT DOMAIN 3928 3966 LDL-RECEPTOR CLASS A 36.
FT DOMAIN 3968 4008 EGF-LIKE 14.
FT DOMAIN 4009 4050 EGF-LIKE 15.
FT DOMAIN 4156 4197 LDL-RECEPTOR CLASS B 35.
FT DOMAIN 4199 4241 LDL-RECEPTOR CLASS B 36.
FT DOMAIN 4244 4284 LDL-RECEPTOR CLASS B 37.
FT DOMAIN 4332 4370 EGF-LIKE 16.
FT DOMAIN 4379 4413 EGF-LIKE 17.
FT DOMAIN 4454 4460 SH3-BINDING (POTENTIAL).
FT DOMAIN 4463 4463 SH3-BINDING (POTENTIAL).
FT DOMAIN 4606 4609 SH2-BINDING (POTENTIAL).
FT DOMAIN 4619 4625 SH3-BINDING (POTENTIAL).
FT DOMAIN 4624 4630 SH3-BINDING (POTENTIAL).
FT DOMAIN 4632 4632 CELL ATTACHMENT SITE (POTENTIAL).
FT DOMAIN 4527 4527 ENDOCYTOSIS SIGNAL (POTENTIAL).
FT DOMAIN 4601 4606 ENDOCYTOSIS SIGNAL (POTENTIAL).
FT DOMAIN 28 40 BY SIMILARITY.
FT DOMAIN 35 53 BY SIMILARITY.
FT DOMAIN 47 62 BY SIMILARITY.
FT DOMAIN 67 80 BY SIMILARITY.
FT DOMAIN 74 93 BY SIMILARITY.
FT DOMAIN 87 103 BY SIMILARITY.
FT DOMAIN 108 120 BY SIMILARITY.
FT DOMAIN 115 133 BY SIMILARITY.
FT DOMAIN 127 142 BY SIMILARITY.
FT DOMAIN 147 157 BY SIMILARITY.

Query Match 9.0%; Score 82; DB 1; Length 4660;
Best Local Similarity 25.8%; Pred. No. 15;
Matches 40; Conservative 15; Mismatches 64; Indels 36; Gaps 8;

```

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Qy 33 SCPEBYR-WPILATGTCMCKTTCNHQ---SORTCAAFCSLSCKREOGKFTYH----- 81
Db 3076 TCPLHQPCDN--GHCIEMGRVCNHYDDCSDNSDEKGGINECLDSISIRCHNCTDTIT 3133
Qy 82 -----LLRDCISCAST--CGOHPKOCAYFCENCGRSPV-NLPPELARORSGEVE 127
Db 3134 SFYSCGLGKYLMSKRCVVDIDECKESBQDCSGKCENVVSGYICKACAPGYIREPDGASC 3193
Qy 128 NNSDN-----SGRY--QGLEHRSSEASPALPGL 153

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Db 3194 RQNSNIEPPLIFSNRYIRLITDSSSYSLQGL 3228
RESULT 10
ID RECK_HUMAN STANDARD; PRT; 971 AA.
AC O95980; Q8WX37;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Reversion-inducing cysteine-rich protein with Kazal motifs precursor
DE (RECK) (Suppressor of tumorigenicity 15) (ST15).
GN RECK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Fibroblast;
RX MEDLINE=99007295; PubMed=9789069;
RA Takahashi C., Sheng Z., Horan T.P., Kitayama H., Maki M., Hitomi K.,
RA Kitaura Y., Takai S., Sasahara R.M., Hojimoto A., Ikawa Y.,
RA Ratzkin B.J., Arakawa T., Noda M.;
RT "Regulation of matrix metalloproteinase-9 and inhibition of tumor
RL invasion by the matrix metalloproteinase-anchored glycoprotein RECK.";
Proc. Natl. Acad. Sci. U.S.A. 95:13321-13326(1998).
RN [2]
RP SEQUENCE OF 363-971 FROM N.A.
RA Kimberley A.;
RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL -1- FUNCTION: Negatively regulates matrix metalloproteinase-9 (MMP-9)
CC by suppressing MMP-9 secretion and by direct inhibition of its
CC enzymatic activity. RECK down-regulation by oncogenic signals may
CC facilitate tumor invasion and metastasis. Appears to also
CC regulate MMP-2 and MT1-MMP, which are involved in cancer
CC progression.
CC -1- SUBUNIT: Interacts with MMP-9.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- TISSUE SPECIFICITY: Expressed in various tissues and untransformed
CC cells. It is undetectable in tumor-derived cell lines and
CC oncogenically transformed cells.
CC -1- SIMILARITY: CONTAINS 3 KAZAL-LIKE DOMAINS.
CC
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CC or send an email to license@ebi.ac.uk.)
CC
CC -----
CC EMBL; D50406; BAA34060.1; -.
CC GenBank; AL158830; CAD13384.1; -.
CC EMBL; HGNC:11345; RECK.
CC MIM; 605227; -.
CC HSPD; P80424; IAN1.
CC InterPro; IPR002350; Kazal.
CC SMART; SM00280; KAZAL; 3.
CC SMART; SM00011; VWC def; 1.
CC PROSITE; PS00282; KAZAL; 1.
CC Signal; Glycoprotein; GPI-anchor; Serine protease inhibitor;
CC Membrane; Anti-oncogene; Repeat.
CC SIGNAL 1 22 POTENTIAL.
CC CHAIN 23 942 REVERSION-INDUCING CYSTEINE-RICH PROTEIN
CC WITH KAZAL MOTIFS.
CC REMOVED IN MATURE FORM (POTENTIAL).
CC LIPID 943 971 KAZAL-LIKE 1.
CC DOMAIN 942 942 KAZAL-LIKE 1.
CC DOMAIN 942 942 KAZAL-LIKE 2 (DEGENERATE).
CC DOMAIN 708 750 KAZAL-LIKE 3 (DEGENERATE).
CC DOMAIN 753 787 5 X KNOT REPEATS.
CC FT 37 338

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FT REPEAT 37 84 KNOT 1.
FT REPEAT 141 141 KNOT 2.
FT REPEAT 104 197 KNOT 3.
FT REPEAT 216 263 KNOT 4.
FT REPEAT 292 338 KNOT 5.
FT DISULFID 635 654 BY SIMILARITY.
FT DISULFID 633 658 BY SIMILARITY.
FT DISULFID 677 693 BY SIMILARITY.
FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 971 AA, 106456 MW, 173D47D6AE6F834 CRC64;

Query Match 8.9%; Score 81; DB 1; Length 971;
Best Local Similarity 21.8%; Pred. No. 3.9;
Matches 32; Conservative 18; Mismatches 41; Indels 56; Gaps 8;

QY 34 CPEE-QYWDPL-----LQTC-----MSCKTICNHQSQRTCAFCRSIS 70
DB 74 CPEIWEIWNKMSLPGVFKKSDGVNGGCCCLATALECRQCKQASSKNDI----SKY 129
QY 71 CRKQCKFDFDLRLDCIS-----CASTCGQHPKOCATFCENKLRSPVNLPEELRQRS 123
DB 130 CRKE-----YENMLFSCISIRNEMGVSVCYSAGHR-TVCREYCAIFRT----- 171
QY 124 GEVENNSDNGRYQGLEHRSSEASPAL 150
DB 172 ----DSGSPSQIKAVENYCAISIPOL 194

RESULT 11
TIE2_HUMAN STANDARD; PRT; 1124 AA.
AC 002763;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiopoietin 1 receptor precursor (EC 2.7.1.112) (Tyrosine-protein
DE kinase receptor TIE-2) (Tyrosine-protein kinase receptor TEK) (1140
DE TEK) (hunca interna endothelial cell kinase) (CD202b antigen).
GN TEK OR TIE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISUE=Placenta;
RX MEDLINE=93173509; PubMed=8382358;
RA Ziegler S.F., Bird T.A., Scherlinger J.A., Schooley K.A., Baum P.R.;
RT "Molecular cloning and characterization of a novel receptor protein
RT tyrosine kinase from human placenta."
RL Oncogene 8:663-670(1993).
RN [2]
RN VARIANT VMCM1 TRP-849.
RX MEDLINE=97134665; PubMed=8980225;
RA Vikkula M., Boon L.M., Carraway K.L. III, Calvert J.T., Diamond A.J.,
RA Goumnerov B., Paayk K.A., Marchuk D.A., Waman M.L., Cantley L.C.,
RA Mulliken J.B., Olse B.R.;
RT "Vascular dysmorphogenesis caused by an activating mutation in the
RT receptor tyrosine kinase TIE2."
RL Cell 87:1181-1190(1996).
RN [3]
RP VARIANTS VMCM1 TRP-849 AND SER-897.
RX MEDLINE=9929243; PubMed=10369874;
RA Calvert J.T., Riney T.J., Kontos C.D., Cha E.H., Prieto V.G.,
RA Shea C.R., Berg J.N., Nevlin N.C., Simpson S.A., Paayk K.A.,
RA Spear M.C., Peters K.G., Marchuk D.A.;
RT "Allelic and locus heterogeneity in inherited venous malformations";
RT Hum. Mol. Genet. 8:1279-1289(1999).
CC -1- FUNCTION: THIS PROTEIN IS A PROTEIN TYROSINE-KINASE TRANSMEMBRANE

```

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CC RECEPTOR FOR ANGIOPOIETIN 1. IT MAY CONSTITUTE THE EARLIEST
CC MAMMALIAN ENDOTHELIAL CELL LINEAGE MARKER. PROBABLY REGULATES
CC ENDOTHELIAL CELL PROLIFERATION, DIFFERENTIATION AND GUIDES THE
CC PROPER PATTERNING OF ENDOTHELIAL CELLS DURING BLOOD VESSEL
CC FORMATION.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN ENDOTHELIAL CELLS
CC AND THEIR PROGENITORS, THE ANGIOBLASTS. HAS BEEN DIRECTLY FOUND
CC IN PLACENTA AND LUNG, WITH A LOWER LEVEL IN UMBILICAL VEIN
CC ENDOTHELIAL CELLS, BRAIN AND KIDNEY.
CC -1- DISEASE: DEFECTS IN TEK ARE A CAUSE OF DOMINANTLY INHERITED VENOUS
CC MALFORMATIONS (VMCM1), AN ERROR OF VASCULAR MORPHOGENESIS
CC CHARACTERIZED BY DILATED, SERPIGINOUS CHANNELS.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. THE
CC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- DATABASE: NAME=PROV, NOTE=PROV 3:12-14(2002);
CC WWW="http://www.ncbi.nlm.nih.gov/prov/guide/1715848914_g.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L06139; AAA61139.1; -.
CC HSSP: P11362; IFGK.
CC Genew: HGNC:11724; TEK.
CC MIM: 600221; -.
CC MIM: 600195; -.
CC InterPro: IPR000561; EGF-like.
CC InterPro: IPR000719; Euk_pkinase.
CC InterPro: IPR003961; FN_III.
CC InterPro: IPR001245; Tyr_pkinase.
CC Pfam: PF00008; EGF_1.
CC Pfam: PF00041; fn3; 3.
CC Pfam: PF00069; pkinase; 1.
CC PRINTS: PR00109; TYRKINASE.
CC ProDom: PD000001; Euk_pkinase; 1.
CC SMART: SMO0181; EGF_2.
CC SMART: SMO0001; EGF-like; 1.
CC SMART: SMO0060; FN3; 3.
CC SMART: SMO0219; Tyrc; 1.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
CC PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
CC PROSITE: PS00022; EGF_1; 3.
CC PROSITE: PS01186; EGF_2; 3.
CC Repeat: Tyrosine-protein kinase; Transferase; Signal; ATP-binding;
CC Repeat; EGF-like domain; Transmembrane; Immunoglobulin domain;
CC Glycoprotein; Phosphorylation; Multigene family; Disease mutation.
CC SIGNAL 1 18
CC CHAIN 19 1124 ANGIOPOIETIN 1 RECEPTOR.
CC DOMAIN 19 745 EXTRACELLULAR (POTENTIAL).
CC TRANSSEM 746 770 POTENTIAL.
CC DOMAIN 771 1124 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 44 102 IG-LIKE C2-TYPE DOMAIN 1.
CC DOMAIN 210 252 EGF-LIKE 1.
CC DOMAIN 254 299 EGF-LIKE 2.
CC DOMAIN 301 341 EGF-LIKE 3.
CC DOMAIN 424 424 IG-LIKE C2-TYPE DOMAIN 2.
CC DOMAIN 444 536 FIBRONECTIN TYPE-III 1.
CC DOMAIN 541 634 FIBRONECTIN TYPE-III 2.
CC DOMAIN 638 732 FIBRONECTIN TYPE-III 3.
CC DOMAIN 824 1096 PROTEIN KINASE.
CC NP_BIND 830 838 ATP (BY SIMILARITY).
CC BINDING 855 855 ATP (BY SIMILARITY).

```


RA Pulkkinen L., Gerecke D.R., Christiano A.M., Wagman D.W.,
RA Burgeson R.E., Uitto J.;
RT "Cloning of the beta 3 chain gene (LAMB3) of human laminin 5, a
RT candidate gene in junctional epidermolysis bullosa.";
RL Genomics 25:192-198(1995).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 172-190.
RX MEDLINE=94209274; PubMed=7512558;
RA Gerecke D.R., Wagman D.W., Champilaud M.F., Burgeson R.E.;
RT "The complete primary structure for a novel laminin chain, the
RT laminin Bk chain.";
RL J. Biol. Chem. 269:11073-11080(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=2121101; PubMed=11296269;
RA Robbins P.B., Lin Q., Goodnough J.B., Tian H., Chen X., Khavari P.A.;
RT "In vivo restoration of laminin 5 beta 3 expression and function in
RT functional epidermolysis bullosa.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:5193-5198(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Epidermis;
RX MEDLINE=96015057; PubMed=8530036;
RA Morishima Y., Arizawa T., Yamashita K., Abe T., Ueda E., Yasuno H.,
RA Inazawa J.;
RT "Chromosomal loci of 50 human keratinocyte cDNAs assigned by
RT fluorescence in situ hybridization.";
RL Genomics 28:273-279(1995).
RN [5]
RP SEQUENCE FROM N.A.
RA Graefen D.;
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
RN [6]
RP VARIANT JEB LEU-679.
RX MEDLINE=96055522; PubMed=7550237;
RA Pulkkinen L., McGrath J.A., Christiano A.M., Uitto J.;
RT "Detection of sequence variants in the gene encoding the beta 3 chain
RT of laminin 5 (LAMB3).";
RL Hum. Mutat. 6:77-84(1995).
RN [7]
RP VARIANT GABEB LYS-210.
RX MEDLINE=99068967; PubMed=9767254;
RA Mellerio J.E., Eady R.A., Atherton D.J., Lake B.D., McGrath J.A.;
RT "E210K mutation in the gene encoding the beta3 chain of laminin-5
RT (LAMB3) is predictive of a phenotype of generalized atrophic benign
RT epidermolysis bullosa.";
RL Br. J. Dermatol. 139:325-331(1998).
CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration, and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end.
CC THE BETA-3 CHAIN IS A SUBUNIT OF LAMININ-5 (EPILGRIN/KALININ/
CC NICEIN).
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
CC COMPONENT).
CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC -1- DOMAIN: DOMAIN VI IS GLOBULAR.
CC -1- DISEASE: DEFECTS IN LAMB3 ARE A CAUSE OF JUNCTIONAL EPIDERMOLYSIS
CC BULLOSA (JEB GRAVIS), ALSO KNOWN AS HERLITZ TYPE JEB. IT IS A
CC BLISTERING DISORDER IN SKIN THAT IS CHARACTERIZED BY A SEPARATION
CC OF BASAL CELLS FROM THE BASEMENT MEMBRANE DUE TO A DECREASED
CC NUMBER OF HEMIDESMOSOMES. LAMININ-5 IS MISSING FROM THE BASEMENT
CC MEMBRANE OF PATIENTS WITH THE GRAVIS FORM OF EPIDERMOLYSIS
CC BULLOSA.
CC -1- DISEASE: DEFECTS IN LAMB3 ARE A CAUSE OF GENERALIZED ATROPHIC
CC BENIGN EPIDERMOLYSIS BULLOSA (GABEB). THIS NONLETHAL FORM OF

CC JUNCTIONAL EPIDERMOLYSIS BULLOSA IS CHARACTERIZED BY LIFE-LONG
CC BLISTERING OF THE SKIN, ASSOCIATED WITH HAIR AND TOOTH
CC ABNORMALITIES.
CC -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
CC -1- SIMILARITY: CONTAINS 6 LAMININ EGF-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL, U17760; AAC51352.1; -;
CC EMBL, U17745; AAC51352.1; JOINED.
CC EMBL, U17746; AAC51352.1; JOINED.
CC EMBL, U17747; AAC51352.1; JOINED.
CC EMBL, U17748; AAC51352.1; JOINED.
CC EMBL, U17749; AAC51352.1; JOINED.
CC EMBL, U17750; AAC51352.1; JOINED.
CC EMBL, U17751; AAC51352.1; JOINED.
CC EMBL, U17752; AAC51352.1; JOINED.
CC EMBL, U17753; AAC51352.1; JOINED.
CC EMBL, U17754; AAC51352.1; JOINED.
CC EMBL, U17755; AAC51352.1; JOINED.
CC EMBL, U17756; AAC51352.1; JOINED.
CC EMBL, U17757; AAC51352.1; JOINED.
CC EMBL, U17758; AAC51352.1; JOINED.
CC EMBL, U17759; AAC51352.1; JOINED.
CC EMBL, L25541; AA61834.1; -;
CC EMBL, AY035783; AA61364.1; -;
CC EMBL, D37766; BAA2263.1; -;
CC EMBL, AL031316; CAB40149.1; -;
CC EMBL, AL023754; CAA19297.1; -;
CC HSSP, P02468; 1K0.
CC GeneW, HGNC:6490; LAMB3.
CC MIM, 150310; -;
CC MIM, 226650; -;
CC MIM, 226700; -;
CC InterPro, IPR000561; EGF-like.
CC InterPro, IPR001886; LamNT.
CC InterPro, IPR002049; Laminin_EGF.
CC Pfam, PF00053; laminin_EGF_6.
CC Pfam, PF00055; laminin_Nterm_1.
CC PRINTS, PR00011; EGF/LAMININ.
CC ProDom, PD002082; LamNT_1.
CC SMART, SM00180; EGF_Lam_6.
CC SMART, SM00136; LamNT_1.
CC PROSITE, PS00022; EGF_1; 5.
CC PROSITE, PS01186; EGF_2; 1.
CC PROSITE, PS01248; LAMININ TYPE EGF; 5.
CC GlycoProtex, Basement membrane; Extracellular matrix; Coiled coil;
CC Laminin EGF-like domain; Cell adhesion; Repeat; Signal;
CC Disease mutation; Epidermolysis bullosa.
CC KX Laminin EGF-like domain; Cell adhesion; Repeat; Signal;
CC KW Disease mutation; Epidermolysis bullosa.
CC FT SIGNAL 1 17
CC FT CHAIN 18 172
CC FT DOMAIN 18 249
CC FT DOMAIN 250 315
CC FT DOMAIN 316 378
CC FT DOMAIN 379 430
CC FT DOMAIN 431 480
CC FT DOMAIN 481 533
CC FT DOMAIN 534 578
CC FT DOMAIN 579 785
CC FT DOMAIN 786 816
CC FT DOMAIN 817 1170
CC FT DOMAIN 723 1170
CC FT DOMAIN 831 884
CC FT DOMAIN 948 1133
CC FT DISULFD 250 259
CC FT DISULFD 252 279
CC FT DISULFD 281 290
CC LAMININ BETA-3 CHAIN.
CC LAMININ N-TERMINAL (DOMAIN VI).
CC LAMININ EGF-LIKE 1.
CC LAMININ EGF-LIKE 2.
CC LAMININ EGF-LIKE 3.
CC LAMININ EGF-LIKE 4.
CC LAMININ EGF-LIKE 5.
CC LAMININ EGF-LIKE 6.
CC DOMAIN II.
CC DOMAIN ALPHA.
CC DOMAIN I.
CC COILED COIL (POTENTIAL).
CC COILED COIL (POTENTIAL).
CC COILED COIL (POTENTIAL).
CC BY SIMILARITY.
CC BY SIMILARITY.
CC BY SIMILARITY.

Query Match	Beet Local Similarity	Score	DB	Length
Query Match	Beet Local Similarity	Score	DB	Length
Matches 41; Conservative	25.3%;	79.5;	1;	1172;
	16; Mismatches	66; Indels	39; Gaps	
19 ERPPGGLMTGVAMRSCPEQGYMDPLGLTGMSCSKTICNHQSQRCAFCRSLSC--RKEGG 76				
504 EEPGGLMCAALIKOCPEPTTYGDVATG-----CRACDDEFGTGG 543				
77 KEYDHLRLDPCISASICGQHPKQCAV-FCENKLRSPV-----NLPEELRRQ--RSG 124				
544 PCQDKASGRCLORPGLTGRCDQCQGYCN---RYVVCVAACHPCPOTYADLRQQLRRG 600				
125 EYENNSDNGSRVQGLHRSSEASPALPGLKLSADQVALVYST 166				
601 RLRLNATASLMSGPELDRGL-ASRLIDA-KSKIEQIRAVLSS 640				
RESULT 14				
YL DROME	STANDARD;	PRT;	1984 AA.	
ID YL DROME				
AC P98163;				
DT 01-OCT-1996 (Rel. 34, Last sequence update)				
DT 01-OCT-1996 (Rel. 34, Last sequence update)				
DT 15-JUN-2002 (Rel. 41, Last annotation update)				
DE Putative vitellogenin receptor precursor (YL).				
GN YL OR YOLKLESS.				
OS Drosophila melanogaster (Fruit fly).				
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;				
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachyera;				
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.				
OK NCBI_taxid=7227;				
RN [1]				
SEQUENCE FROM N.A.				

[illegible]

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FT DISULFID 129 144 BY SIMILARITY.
FT DISULFID 137 157 BY SIMILARITY.
FT DISULFID 151 166 BY SIMILARITY.
FT DISULFID 184 197 BY SIMILARITY.
FT DISULFID 191 210 BY SIMILARITY.
FT DISULFID 204 220 BY SIMILARITY.
FT DISULFID 227 239 BY SIMILARITY.
FT DISULFID 234 253 BY SIMILARITY.
FT DISULFID 247 262 BY SIMILARITY.
FT DISULFID 266 281 BY SIMILARITY.
FT DISULFID 275 294 BY SIMILARITY.
FT DISULFID 288 304 BY SIMILARITY.
FT DISULFID 310 321 BY SIMILARITY.
FT DISULFID 315 331 BY SIMILARITY.
FT DISULFID 333 346 BY SIMILARITY.
FT DISULFID 352 363 BY SIMILARITY.
FT DISULFID 359 372 BY SIMILARITY.
FT DISULFID 374 387 BY SIMILARITY.
FT DISULFID 664 673 BY SIMILARITY.
FT DISULFID 669 685 BY SIMILARITY.
FT DISULFID 687 700 BY SIMILARITY.
FT DISULFID 988 999 BY SIMILARITY.
FT DISULFID 995 1009 BY SIMILARITY.
FT DISULFID 1011 1025 BY SIMILARITY.
FT DISULFID 1031 1040 BY SIMILARITY.
FT DISULFID 1035 1053 BY SIMILARITY.
FT DISULFID 1047 1062 BY SIMILARITY.
FT DISULFID 1074 1087 BY SIMILARITY.
FT DISULFID 1081 1100 BY SIMILARITY.
FT DISULFID 1094 1109 BY SIMILARITY.
FT DISULFID 1118 1130 BY SIMILARITY.
FT DISULFID 1125 1143 BY SIMILARITY.
FT DISULFID 1137 1152 BY SIMILARITY.
FT DISULFID 1158 1170 BY SIMILARITY.
FT DISULFID 1165 1183 BY SIMILARITY.
FT DISULFID 1177 1193 BY SIMILARITY.
FT DISULFID 1198 1210 BY SIMILARITY.
FT DISULFID 1215 1232 BY SIMILARITY.
FT DISULFID 1217 1232 BY SIMILARITY.
FT DISULFID 1243 1257 BY SIMILARITY.
FT DISULFID 1250 1270 BY SIMILARITY.
FT DISULFID 1264 1279 BY SIMILARITY.
FT DISULFID 1283 1296 BY SIMILARITY.
FT DISULFID 1290 1309 BY SIMILARITY.
FT DISULFID 1303 1318 BY SIMILARITY.
FT DISULFID 1340 1352 BY SIMILARITY.
FT DISULFID 1347 1365 BY SIMILARITY.
FT DISULFID 1359 1375 BY SIMILARITY.
FT DISULFID 1379 1392 BY SIMILARITY.
FT DISULFID 1401 1416 BY SIMILARITY.
FT DISULFID 1403 1416 BY SIMILARITY.
FT DISULFID 1422 1432 BY SIMILARITY.
FT DISULFID 1428 1441 BY SIMILARITY.
FT DISULFID 1443 1456 BY SIMILARITY.
FT DISULFID 1738 1747 BY SIMILARITY.
FT DISULFID 1743 1756 BY SIMILARITY.
FT DISULFID 1758 1769 BY SIMILARITY.
FT CARBOHYD 30 30 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 429 429 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 666 666 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 749 749 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 782 782 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1022 1022 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1240 1240 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1265 1265 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1326 1326 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1475 1475 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1490 1490 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 1519 1519 V -> I.
SQ SEQUENCE 1984 AA; 219318 MW; F92A256B0ACD5E48 CRC64;

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Query Match 8.7%; Score 79.5; DB 1; Length 1984;
Best Local Similarity 29.9%; Pred. No. 11;
Matches 32; Conservative 7; Mismatches 41; Indels 27; Gaps 8;

Qy 26 WTGVAMRSCPEEQVMDPLGTCMSCKTCN-----HQSRTCAACRSIS----- 70
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1333 WS-TSSRSC-RPHLPDQDECDVLSRVCCNFPDCTNGHDSGPKATYCRSASGQVCOH 1390
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 71 -CRKEQG---KFVD--HLNRDCISGASI--CGQHPKOCAYPCENKL 108
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1391 KCRATPAGAVCSCFPGYRLDNDQKSCLDIDEC-QEQPCAOUCENTLL 1436
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
ID 2147 HUMAN STANDARD; PRT; 630 AA.
AC 014258;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Zinc finger protein 147 (Estrogen responsive finger protein) (Efp).
GN ZNF147 OR EFP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=9406555; PubMed=8248217;
RA Inoue S., Oriimo A., Hosoi T., Kondo S., Toyoshima H., Kondo T.,
RA Ikegami A., Ouchi Y., Oriimo H., Muramatsu M.;
RT "Genomic binding-site cloning reveals an estrogen-responsive gene that
RT encodes a Ring finger protein."
RC Proc. Natl. Acad. Sci. U.S.A. 90:11117-11121(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Straubeberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC - FUNCTION: MEDIATES ESTROGEN ACTION IN VARIOUS TARGET ORGANS.
CC - TISSUE SPECIFICITY: UBICUITOUS.
CC - SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC - SIMILARITY: CONTAINS 1 SPRY DOMAIN.
-----
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DR EMBL; D21205; BA04747.1; -.
DR EMBL; BC016924; AAH16924.1; -.
DR GenBank; HGNC:12932; ZNF147.
DR MIM; 600453; -.
DR InterPro; IPR001870; Gamma_carboxylase.
DR InterPro; IPR003878; SPRY_domain.
DR InterPro; IPR003877; SPRY_receptor.
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00097; ZF-C3HC4; 1.
DR Pfam; PF00622; SPRY; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR Zinc-finger; Coiled-coil.
FT ZN FING 13 54 RING-TYPE.
FT DOMAIN 217 307 COILED COIL (POTENTIAL).
FT DOMAIN 509 630 SPRY.
SQ SEQUENCE 630 AA; 70989 MW; BE4EE713F96DD080 CRC64;

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Query Match 8.6%; Score 78.5; DB 1; Length 630;
Best Local Similarity 23.0%; Pred. No. 4.4;
Matches 38; Conservative 20; Mismatches 54; Indels 53; Gaps 9;

QY 22 PQGLMTGVAMSGPBEQYWDPIILGTOMSKTICNH-----QSQRTC-----AARCRS-LSCR 72
Db 86 PADVTPPPARASAPSP-----NAQVACDHCLKEAAVKTCLVCMASFQGEHLOPH 134
QY 73 KEQGFYDHL-----RDCISCASICGHPKQCAVFC-----ENKLRSPVNL 115
Db 135 FDSPPAFQDHPLOHPVRDL--RRKCSQHNRLEFFCPHSEICICLVEHKTCSPASL- 191
QY 116 PELRRQSGEVENNSDNGRYQGLHRSSEASPALPGLKLSADQV 160
Db 192 ---SQASADLEAT-----LRHKLTVMTYSQINGASRALDV 223

Search completed: February 4, 2003, 12:58:12
Job time : 14.4251 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 4, 2003, 12:56:21 / Search time 19.4899 Seconds
(without alignments)
818.800 Million cell updates/sec

Title: US-09-854-864-15

Perfect score: 909

Sequence: 1 MSGIGRRRRGGRSRVDOEER.....SPALPGKLSADQVALVYST 166

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97.5	10.7	1548	2	S34583
2	86.5	9.5	353	2	T06466
3	86	9.5	1299	2	T43251
4	84.5	9.3	355	2	AD0299
5	83	9.1	13288	2	T03099
6	82.5	9.1	899	2	G02428
7	82.5	9.1	915	2	JC6148
8	82	9.0	932	2	T52527
9	82	9.0	1650	2	S53457
10	82	9.0	4660	2	T42737
11	81	8.9	773	1	JH0609
12	81	8.9	1124	1	I58388
13	80.5	8.9	937	2	I53282
14	80	8.8	108	2	H69834
15	80	8.8	330	2	T25169
16	80	8.8	996	2	JB0237
17	79.5	8.7	1984	2	T13171
18	79	8.7	269	2	CE9312
19	78.5	8.6	630	2	A49656
20	78.5	8.6	1170	2	A53612
21	78	8.6	596	2	A45664
22	77.5	8.5	230	2	T19364
23	77.5	8.5	2195	2	T34264
24	77.5	8.5	2871	2	A55624
25	77	8.5	620	2	AF0273
26	77	8.5	751	2	T15230
27	77	8.5	1184	2	T09484
28	76.5	8.4	1680	2	A43434
29	76.5	8.4	1872	2	JC4976

30 76 8.4 367 2 T45812
31 76 8.4 574 2 B88465
32 76 8.4 915 2 B48225
33 76 8.4 1748 2 S42136
34 75.5 8.3 427 2 S38032
35 75.5 8.3 1620 2 T27283
36 75 8.3 962 2 JC5571
37 75 8.3 969 2 A39490
38 75 8.3 975 2 JC5570
39 75 8.3 2664 2 T28626
40 75 8.3 3002 2 A47221
41 75 8.3 4544 1 S02392
42 75 8.3 4545 1 S25111
43 74.5 8.2 382 1 S48748
44 74.5 8.2 501 2 T61512
45 74.5 8.2 773 2 I46059

ALIGNMENTS

RESULT 1
S34583
serine proteinase (EC 3.4.21.-) PC6B - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C:Accession: S34583
R:Nakagawa, T.; Murakami, K.; Nakayama, K.
FEBS Lett. 327, 165-171, 1993
A>Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a
A:Reference number: S34583; MUID:93327934; PMID:8335106
A:Accession: S34583
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1548 <NA>
A:Cross-references: GB:DI7563; NID:g407344; PIDN:BAA04507.1; PID:d1005033; PID:g440374
C:Keywords: hydrolase; serine proteinase

Query Match 10.7%; Score 97.5; DB 2; Length 1548;
Best Local Similarity 30.2%; Pred. No. 1;
Matches 29; Conservative 12; Mismatches 32; Indels 23; Gaps 7;

QY 14 RVDQ--EERFPGIMTVGVMRSCEEQYWDPLG-TCMSCKTICN-----HQSGRTCAAF 65
DB 627 RADKKGGRF---LYHSGCLENCVPGHY--PAKGTGCLPCPDNCLCVNPHICRSMGCV 681
QY 66 -----CRSLSCKEQCKFTYDHLRDCISCASIC 93
DB 682 VIIPNHTCKLECR--QGEFQDSEYECWPCCEEGC 715

RESULT 2
T06466
cathepsin B-like cysteine proteinase (EC 3.4.22.-) (clone A116) - wheat (fragment)
C:Species: Triticum aestivum (common wheat)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C:Accession: T06466
R:Cejudo, F.J.; Murphy, G.; Chirnov, C.; Baulcombe, D.C.
Plant J. 2, 937-948, 1992
A>Title: A gibberellin-regulated gene from wheat with sequence homology to cathepsin B c
A:Reference number: Z15659; MUID:93258430; PMID:1302642
A:Accession: T06466
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-953 <CEU>
A:Cross-references: EMBL:X66013; NID:g21698; PIDN:CAA46811.1; PID:g21699
A:Experimental source: cv. Chinese Spring, etiolated shoots
C:Genetics:
A>Note: Intron positions not resolved (incomplete sequence)
C:Superfamily: papain
C:Keywords: cysteine proteinase; glycoprotein; hydrolase

Query Match 9.5%; Score 86.5; DB 2; Length 353;

Best Local Similarity 24.7%; Pred. No. 2.7;
Matches 36; Conservative 12; Mismatches 63; Indels 35; Gaps 5;

Qy 22 PGLMTGVMARSCPE-----EQYMDPLGTGCMSCKTTICNHOSQRTCAAFCRSLSCR 72
Db 80 PGLMTGVMARSCPE-----EQYMDPLGTGCMSCKTTICNHOSQRTCAAFCRSLSCR 132
Qy 73 KEQKRYVDHL-----LRDLCISCAICGHPKQCAVFCENKLRSPVNLPELRRORSGE 125
Db 133 ALQDRFCIHLNMSVSLVNDLLAC-----CGFLCGSGNGGVPISAWYFRRSKV 182
Qy 126 VENNNDNSGRVQGLEHRSSEASPALP 151
Db 183 VTRECDPYEDQTCQHPGCE--PAYP 206

RESULT 3

T43251
Furin (EC 3.4.21.75) - fall armyworm

N/Alternate names: paired basic amino acid cleaving enzyme; proprotein convertase; serin
C/Species: Spodoptera frugiperda (fall armyworm)
C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000

C/Accession: T43251
R/Cleptik, M.; Klenk, H.
Submitted to the EMBL Data Library, January 1996

A/Description: Cloning and functional characterization of FURIN from Spodoptera frugiper
A/Reference number: 222368

A/Accession: T43251
A/Status: preliminary; translated from GB/EMBL/DBDJ

A/Molecule type: mRNA
A/Residues: 1-1299 <CIB>
A/Cross-references: EMBL:268888; NID:g1167859; PID:e219690; PIDN:CAA93116.1

A/Experimental source: clone sfurin 6; ovary
C/Function:
A/Description: responsible for the endoproteolytic processing of proproteins with specif
C/Keywords: hydrolase; serine proteinase

Query Match 9.5%; Score 86; DB 2; Length 1299;
Best Local Similarity 25.0%; Pred. No. 9.2;
Matches 39; Conservative 16; Mismatches 51; Indels 50; Gaps 9;

Qy 22 PGLMTGVMARSCPEEQYMDPLGTGCMSCKTTICNHOSQRTCAAFCRSLSCRKEQKRF--- 78
Db 1104 PRLMDGGLCMECLGQYDVSATGTCRSCDASC-----PGQFSCCT 1148
Qy 79 -----YHLLRDCISCAICG---QHPKQCAVFCENKLRSPVNLPELRRORSGEYE 127
Db 1149 TCSRPLRIRLNNQCVPCSEKGVMTSTPTDCH-CN-----DE-----NGECL 1192
Qy 128 NNSDNGRYQGLEHRSSEASPALPGLKLSADQVALV 163
Db 1193 NSS-VAGKRRIAEWGLAHTAPASD-----AAPSAVVV 1223

RESULT 4

AD0299
conserved hypothetical protein YPO2451 [imported] - Yersinia pestis (strain CO92)

C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001

C/Accession: AD0299
R/Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tlball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Crofton, A.; Davies, R.M.; Dougan, G.;

11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001

A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360

A/Accession: AD0299
A/Status: preliminary

A/Molecule type: DNA
A/Residues: 1-355 <KUR>

A/Cross-references: GB:AL550842; PIDN:CA091256.1; PID:g15980445; GSPDB:GN00175
A/Genetic:
A/Gene: YPO2451

C/Superfamily: Escherichia coli ycea protein

Query Match 9.3%; Score 84.5; DB 2; Length 355;
Best Local Similarity 24.4%; Pred. No. 4;
Matches 30; Conservative 20; Mismatches 48; Indels 25; Gaps 5;

Qy 37 EQYMDPLGTGCMSCKTTICNHOSQRTCAAFCRSLSCRKEQKRYVDHLRDCISCAICGQH 96
Db 257 ERISDDVIAHQCGTTPCADHTN-----CKNDG-----HLT--FIQCPVCAAKF 299
Qy 97 PKQCAVFCENKLRSPVNLPELRRORSGEVENNSDNGRYQGLEHRSSEASPALPGLKLS 156
Db 300 EECGSGTICQEBLK---LPQEBQRPRAGRENGIKIFNKSGL---LQATWHIPSPKS 351
Qy 157 ADQ 159
Db 352 ADB 354

RESULT 5

T03099
mucin, submaxillary - pig

N/Alternate names: apomucin
C/Species: Sus scrofa domestica (domestic pig)

C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Jun-2000
C/Accession: T03099; A40009; A28528; B29789

R/Eckhardt, A.E.; Timpke, C.S.; Deluca, A.W.; Hill, R.L.
J. Biol. Chem. 272, 33204-33210, 1997

A/Title: The complete cDNA sequence and structural polymorphism of the polypeptide chain
A/Reference number: 214839; MUID:98070526; PMID:9407109

A/Accession: T03099
A/Status: preliminary; translated from GB/EMBL/DBDJ

A/Molecule type: mRNA
A/Residues: 1-13288 <ECK>

A/Cross-references: EMBL:AF005273; NID:g2581863; PIDN:AA062527.1; PID:g2581864
R/Eckhardt, A.E.; Timpke, C.S.; Abernethy, J.L.; Zhao, Y.; Hill, R.L.
J. Biol. Chem. 266, 9678-9686, 1991

A/Title: Porcine submaxillary mucin contains a cysteine-rich, carboxyl-terminal domain in
A/Reference number: A40009; MUID:91236743; PMID:2033060

A/Accession: A40009
A/Molecule type: mRNA

A/Residues: 12139-12167, 'T', 12169-13288 <EC3>
A/Cross-references: GB:M21174; GB:003512; NID:g164321; PIDN:AAA30998.1; PID:g164374

R/Timpke, C.S.; Eckhardt, A.E.; Abernethy, J.L.; Hill, R.L.
J. Biol. Chem. 263, 1081-1088, 1988

A/Title: Porcine submaxillary gland apomucin contains tandemly repeated, identical seque
A/Reference number: A28528; MUID:88087170; PMID:2826455

A/Accession: A28528
A/Molecule type: mRNA

A/Residues: 12139-12167, 'T', 12169-12641 <TIM>
A/Cross-references: GB:M21174; GB:003512; NID:g164321; PIDN:AAA30990.1; PID:g552360

A/Experimental source: submaxillary gland
R/Eckhardt, A.E.; Timpke, C.S.; Abernethy, J.L.; Tounadje, A.; Johnson Jr., W.C.; Hill,
J. Biol. Chem. 262, 11339-11344, 1987

A/Title: Structural properties of porcine submaxillary gland apomucin.
A/Reference number: A92606; MUID:87280230; PMID:3611111

A/Accession: B29789
A/Molecule type: protein

A/Residues: 1572-1607 <EC2>
C/Superfamily: pig submaxillary mucin

C/Keywords: tandem repeat

Query Match 9.1%; Score 83; DB 2; Length 13288;
Best Local Similarity 23.5%; Pred. No. 1.3e+02;
Matches 32; Conservative 18; Mismatches 44; Indels 42; Gaps 8;

Qy 18 EERFPGMLTGVAMR-SCPEEQYMD-----PLATGCMSCKTTICNHOSQRTCAAFCRSL 70
Db 13075 BEKSPGDVWTANCHCTGTAKTVDCKRKEGSPPTCTGTERGLIFKXANDTC---CBIGH 13131
Qy 71 CRK-----EGKRYVDHLRDCI--SCAST-----CGQH-----PKQ 99
Db 13132 CEKRTCLFNNTDYEVSFDDPNNPCVTYSCONTGFTAVVONCPKQTCABEDRVYDSKO 13191

QY 100 CAYFENKLR-SPYNL 114
Db 13192 CCYTKSSCKSPYNNV 13207

RESULT 6

G02428
subtilisin-like protease (EC 3.4.21.-) 5 precursor - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Mar-2000
C/Accession: G02428
R/Releaser: T.L.
submitted to the EMBL Data Library, February 1996
A/Reference number: H01442
A/Accession: G02428
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-899 <REU>
A/Cross-references: EMBL:U09114; NID:G1218057; PIDN:AAA91807.1; PID:G1218058
C/Genetics:
A/Status: PCS
C/Keywords: hydrolase, serine proteinase
F/148-386/Domain: subtilisin homology <SBT>

Query Match 9.1%; Score 82.5; DB 2; Length 899;
Best Local Similarity 26.0%; Pred. No. 14;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;

QY 27 TGVAMRSCPEBQYWDPLIGTSCMTICNHOSQRTCAAF-----CR-----SLSC 71
Db 703 TNSCVTHCPDGSYQDTKKNLCRKSENC-----KTCTEFHNCTECRDGLSLQSRCSVSC 757

QY 72 RKEGKPYDHLRDLICISASC-----GQHPKQC-----AYCEN 106
Db 758 --EDGRYPNG--QDQPCHRFCATCAGADGCINCTEGYEMD 797

RESULT 7

JC6148
subtilisin-like protease (EC 3.4.21.-) homolog - human
N/Alternate names: PC6A (protease)
C/Species: Homo sapiens (man)
C/Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 22-Jun-1999
C/Accession: JC6148
R/Miranda, L.; Wolf, J.; Pichante, S.; Duke, R.; Franzsoeff, A.
Proc. Natl. Acad. Sci. U.S.A. 93, 7695-7700, 1996
A/Title: Isolation of the human PC6 gene encoding the putative host protease for HIV-1
A/Reference number: JC6148; MUID:96353880; PMID:875538
A/Contents: CEM T-cell
A/Accession: JC6148
A/Molecule type: mRNA
A/Residues: 1-915 <MTR>
A/Cross-references: GB:U56387; NID:G1498312; PIDN:AAC50643.1; PID:G1498313
C/Comment: This protein functions as a soluble enzyme within the secretory pathway. It is
C/Genetics:
A/Status: PCS
C/Keywords: subtilisin-like proteinase, hydrolase, serine proteinase
F/144-402/Domain: subtilisin homology <SBT>

Query Match 9.1%; Score 82.5; DB 2; Length 915;
Best Local Similarity 26.0%; Pred. No. 14;
Matches 27; Conservative 10; Mismatches 34; Indels 33; Gaps 7;

QY 27 TGVAMRSCPEBQYWDPLIGTSCMTICNHOSQRTCAAF-----CR-----SLSC 71
Db 719 TNSCVTHCPDGSYQDTKKNLCRKSENC-----KTCTEFHNCTECRDGLSLQSRCSVSC 773

QY 72 RKEGKPYDHLRDLICISASC-----GQHPKQC-----AYCEN 106
Db 774 --EDGRYPNG--QDQPCHRFCATCAGADGCINCTEGYEMD 813

RESULT 8

152527
PAC64A - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
C/Accession: 152527
R/Hosaka, M.; Murakami, K.; Nakayama, K.
Biomed. Res. 15, 383-390, 1994
A/Title: PAC64A is a ubiquitous endoprotease that has similar but not identical substrates
A/Reference number: 152527
A/Accession: 152527
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-932 <RES>
A/Cross-references: GB:D50060; NID:G769700; PIDN:BA08777.1; PID:G769701
C/Status: PCS
C/Keywords: subtilisin-like proteinase, hydrolase, serine proteinase
F/112-410/Domain: subtilisin homology <SBT>

Query Match 9.0%; Score 82; DB 2; Length 932;
Best Local Similarity 25.0%; Pred. No. 16;
Matches 28; Conservative 16; Mismatches 44; Indels 24; Gaps 5;

QY 16 DQERFPGGLMTGVAMRSCPEBQYWDPLIGTSCMTICNHOSQRTCAAFCSLSCK 73
Db 650 DEER-----YTGVCHEPCGDKGCDGNADQCLNCHSLNSKTNKCVSECE----- 696

QY 74 EOGKPYDHLRDLICISASC-----GQHPKQC-----AYCENKLRSPYNNLP 116
Db 697 PLGYFGMAARCRCHKGCYCTGRSPADCLSCRGFYHHTNCTVLCIP 748

RESULT 9

SS3457
dominant autoantigen gp 330 - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 18-Aug-2000
C/Accession: SS3457
R/Jokhadze, G.G.; Oleinikov, A.V.; Kanalas, J.J.; Makker, S.P.
Biochem. J. 305, 711-713, 1995
A/Title: Different molecular forms of rat kidney gp330, the dominant autoantigen of active
A/Reference number: SS3457; MUID:95151000; PMID:7848267
A/Accession: SS3457
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-1650 <OK>
C/Status: PCS
F/29-65/Domain: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding
F/72-106/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F/111-147/Domain: EGF homology <EG1>
F/153-188/Domain: EGF homology <EG2>
F/196-235/Domain: LDL receptor WYTD-containing repeat homology <YW01>
F/236-278/Domain: LDL receptor WYTD-containing repeat homology <YW02>
F/279-329/Domain: LDL receptor WYTD-containing repeat homology <YW03>
F/330-373/Domain: LDL receptor WYTD-containing repeat homology <YW04>
F/374-414/Domain: LDL receptor WYTD-containing repeat homology <YW05>
F/415-457/Domain: LDL receptor WYTD-containing repeat homology <YW06>
F/466-505/Domain: EGF homology <EG3>
F/509-545/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F/550-586/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F/595-631/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F/636-672/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F/679-715/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F/720-755/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F/760-794/Domain: LDL receptor ligand-binding repeat homology <LDL8>
F/799-839/Domain: LDL receptor ligand-binding repeat homology <LDL9>
F/843-879/Domain: LDL receptor ligand-binding repeat homology <LDL10>
F/884-921/Domain: LDL receptor ligand-binding repeat homology <LDL11>
F/929-963/Domain: LDL receptor ligand-binding repeat homology <LDL12>
F/971-1006/Domain: EGF homology <EG4>
F/1012-1048/Domain: EGF homology <EG5>
F/1055-1099/Domain: LDL receptor WYTD-containing repeat homology #status atypical <YW07>

F:1100-1154/Domain: LDL receptor YWTD-containing repeat homology #status atypical <YW08>
F:1155-1188/Domain: LDL receptor YWTD-containing repeat homology #status atypical <YW09>
F:1189-1232/Domain: LDL receptor YWTD-containing repeat homology <YW10>
F:1234-1273/Domain: LDL receptor YWTD-containing repeat homology <YW11>
F:1274-1316/Domain: LDL receptor YWTD-containing repeat homology <YW12>
F:1336-1359/Domain: EGF homology <EG6>

Query Match 9.0%; Score 82; DB 2; Length 1650;
Best Local Similarity 25.8%; Pred. No. 26;
Matches 40; Conservative 15; Mismatches 64; Indels 36; Gaps 8;

Qy 33 SCPEBY-WDPILGTGMSCKTICNHQ---SQTCAFCRSLSRKQKGYDH-----81
Db 71 TCPLHQFRCDN--GHCIEGRVCNHNVDSDSGKCEINCELDSSISRCCHNCTDTT 128
Qy 82 -----LLRDCISGASI--CGQHPKOCAYFCENKLRSPV-NLPPELRORSGEVE 127
Db 129 SYFCGCLPGYKLMDSRSCVDIDECESPOLCSQKCEVVGSYTICKACAGYIREPDGKSC 188
Qy 128 NNSDN-----SGRY--QGLHRGSEASPALPGL 153
Db 189 RONSNIPEYLIIFSNNRYIRNLTTDGSYSLLIQL 223

RESULT 10
T42737
gp330 protein precursor - rat
N:Alternate names: megalin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
C:Accession: T42737
R:Salto, A.; Pietromonaco, S.; Loo, A.K.C.; Farquhar, M.G.
Proc. Natl. Acad. Sci. U.S.A. 91, 9725-9729, 1994
A:Title: Complete cloning and sequencing of rat gp330/megalin, a distinctive member of the A:Reference number: A58173; MUID:95024033; PMID:7937880
A:Accession: T42737
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-4660 <SA1>
A:Cross-references: EMBL:L34049; NID:9561852; PID:9561853; PIDN:AAA51369.1
A:Experimental source: serum Sprague-Dawley; kidney
C:Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding F:1-25/Domain: signal sequence #status predicted <Sig>
F:26-4660/Product: gp330 protein #status predicted <Mat>

Query Match 9.0%; Score 82; DB 2; Length 4660;
Best Local Similarity 25.8%; Pred. No. 63;
Matches 40; Conservative 15; Mismatches 64; Indels 36; Gaps 8;

Qy 33 SCPEBY-WDPILGTGMSCKTICNHQ---SQTCAFCRSLSRKQKGYDH-----81
Db 3076 TCPLHQFRCDN--GHCIEGRVCNHNVDSDSGKCEINCELDSSISRCCHNCTDTT 3133
Qy 82 -----LLRDCISGASI--CGQHPKOCAYFCENKLRSPV-NLPPELRORSGEVE 127
Db 3134 SYFCGCLPGYKLMDSRSCVDIDECESPOLCSQKCEVVGSYTICKACAGYIREPDGKSC 3193
Qy 128 NNSDN-----SGRY--QGLHRGSEASPALPGL 153
Db 3194 RONSNIPEYLIIFSNNRYIRNLTTDGSYSLLIQL 3228

RESULT 11
JH0609
protein-tyrosine-phosphatase (EC 3.1.3.48) P19 - mouse
N:Alternate names: protein-tyrosine-phosphatase PTPY43
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0609; PS0365; PS0366; G61180
R:den Hertog, J.; Pale, C.E.G.M.; Jonk, L.J.C.; Kruijer, W.
Biochem. Biophys. Res. Commun. 184, 1241-1249, 1992
A:Title: Differential expression of a novel murine non-receptor protein tyrosine phosphatase
A:Reference number: JH0609; MUID:92272714; PMID:1590786

A:Accession: JH0609
A:Molecule type: mRNA
A:Residues: 1-773 <DEN>
A:Cross-references: GB:X63440; GB:S6169; NID:9416181; PIDN:CAA45037.1; PID:9416182
A:Experimental source: embryonic carcinoma cell, P19 cell

A:Accession: PS0365
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 88-91, 'G', '93-109, 'G', '112-118, 'S', '120, 'T', '122 <DE2>
A:Experimental source: embryonic carcinoma cell, P19 cell, clone PTP33
A:Accession: PS0369

A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 88-91, 'G', '93-109, 'G', '112-120, 'T', '122 <DE3>
A:Experimental source: embryonic carcinoma cell, P19 cell, clone PTP59
A:Accession: PS0366

A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 88-91, 'K', '94-109, 'A', '112-118, 'S', '120-122 <DE4>
A:Experimental source: embryonic carcinoma cell, P19 cell, clone PTP42
R:Yi, T.; Cleveland, J.L.; Ihle, J.N.
Blood 78, 2222-2228, 1991

A:Title: Identification of novel protein tyrosine phosphatases of hematopoietic cells by A:Reference number: A61180; MUID:92032882; PMID:1932742
A:Accession: G61180

A:Status: not compared with conceptual translation
A:Molecule type: mRNA

C:Comment: This protein is located in the cytoplasm.

C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 12, protein-tyrosine-phosphatase; C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase; F:55-299/Domain: phosphatase catalytic domain #status predicted <PCD>
F:58-282/Domain: protein-tyrosine-phosphatase homology <PPP>

F:231/Active site: Cys (phosphocysteine intermediate) #status predicted
F:237/Binding site: substrate phosphate (Arg) #status predicted

Query Match 8.9%; Score 81; DB 1; Length 773;
Best Local Similarity 25.4%; Pred. No. 16;
Matches 45; Conservative 16; Mismatches 48; Indels 66; Gaps 11;

Qy 37 EGYNPLIG---TMSCKTICNHQSORTCAPCRS--LSRKQKGY-----DH- 81
Db 144 ERYW-PLYGEDPTTFAPPKICENEQART-DYFRTLLERQNSRRLYOPHYVWMPDH 201
Qy 82 -----LLRD-----CISGASICGQHPKOCAY-FCENKLR-----S 110
Db 202 VPSSDSTLDMISLMRKQEHEDVPICHCAGCGRTAICADITWMLAKGIPSEFN 261
Qy 111 PNLPELRORSGEVE-----NNSDNGRYQGLHRGSEASPALP 151
Db 262 VFNLIQEWRTGRHSAVQKEQYELVHRAIQLFENSVMKCF--MEHRRSVVMKLP 316

RESULT 12
I58388
protein-tyrosine kinase (EC 2.7.1.112), receptor type tek precursor - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C:Accession: I58388
R:Ziegler, S.F.; Bird, T.A.; Schneringer, J.A.; Schooley, K.A.; Baum, P.R.
Oncogene 8, 663-670, 1993
A:Title: Molecular cloning and characterization of a novel receptor protein tyrosine kinase
A:Reference number: I58388; MUID:93173509; PMID:8382358
A:Accession: I58388
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1124 <RES>
A:Cross-references: GB:I06139; NID:9292823; PIDN:AAA61139.1; PID:9292824
C:Genetic: GDB:TEK
A:Gene: GDB:TEK
A:Cross-references: GDB:344185; OMIM:600221
A:Map position: 9p21-9p21
C:Function:

A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: protein-tyrosine kinase, receptor type Iie; EGF homology; fibronectin ty
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosph
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-124/Domain: product: protein-tyrosine kinase, receptor type tek #status predicted <MAT>
F;37-104/Domain: immunoglobulin homology <IM>
F;115-117/Region: cell attachment (R-G-D) motif
F;211-251/Domain: EGF homology <EG1>
F;255-298/Domain: EGF homology <EG2>
F;302-340/Domain: EGF homology <EG3>
F;364-426/Domain: immunoglobulin homology <IM2>
F;447-527/Domain: fibronectin type III repeat homology <FN3A>
F;542-625/Domain: fibronectin type III repeat homology <FN3B>
F;638-720/Domain: fibronectin type III repeat homology <FN3C>
F;752-772/Domain: transmembrane #status predicted <TM>
F;822-1099/Domain: protein kinase homology <KIN>
F;830-838/Region: protein kinase ATP-binding motif
F;140,158,399,438,464,560,566,649,691/Binding site: carbohydrate (Asn) (covalent) #statu
F;855,872,964/Active site: Lys, Glu, Asp #status predicted

Query Match 8.9%; Score 81; DB 1; Length 1124;
Best Local Similarity 24.2%; Pred. No. 22;
Matches 39; Conservative 15; Mismatches 63; Indels 44; Gaps 8;

Qy 26 WTGVAMRSCPEBQWDP---LLGTGM-----SKTTICN-HQSQ 59
Db 203 FTPLIVRRC-BAQKGPFCNHLCTACMNNGVCHBDTGECICPPFGMRTCEKACELHTFG 261

Qy 60 RTCAAFCSLSCKEKGKFDHLRDCISCAISCGQHKKQCAFPCENKLRSPVNLPELR 119
Db 262 RTCKERCSCG---DEGCKSYVFCPLDPYGCSCATGKGLQCNCAECH---FGFYGPCK 312

Qy 120 RQRSGEVNNSDNRGRYOGLERHGEASPALPGLKLSADQV 160
Db 313 LRCSG---NNGEMCDRFRQ---GCLCSFGWGLQCEKREGI 345

RESULT 13
153282
gene PACE4 protein - rat

C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 22-Jun-1999
C;Accession: 153282

R;Johnson, R.C.; Darlington, D.N.; Hand, T.A.; Bloomquist, B.T.; Matsui, R.E.
Endocrinology 135, 1178-1185, 1994
A;Title: PACE4, a subtilisin-like endoprotease prevalent in the anterior pituitary and z

A;Reference number: 153282; MUID:94345873; PMID:8070361
A;Accession: 153282
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA
A;Residues: 1-937 <RES>
A;Cross-references: GB:U31894; NID:9496221; PIDN:AAA61987.1; PID:9496222
C;GeneticS:
A;Gene: PACE4
C;Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
F;177-415/Domain: subtilisin homology <SBT>

Query Match 8.9%; Score 80.5; DB 2; Length 937;
Best Local Similarity 24.1%; Pred. No. 21;
Matches 27; Conservative 17; Mismatches 45; Indels 23; Gaps 5;

Qy 16 DOEERFPGMLWTGVAMRSCPEBQWDPPLGTGMSCK--TICNHSQRTCAAFCSLSCKR 73
Db 654 EEEBEY-----TGCHPCGDKGCGPSADQCLNCVHPSLSKSKNRKCVSEC----- 701

Qy 74 EOGKFDYHLRDCISCAISCG---GQHPKQC---AFCEKLRSPVNLPP 116
Db 702 PLGYGDTAARCRCHGKCECTGSRSPFGQCLSCRRGFYHDETNVTCVTLCP 753

RESULT 14
H69834
hypothetical protein yhjQ - Bacillus subtilis

C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C;Accession: H69834

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero
C.; Bron, S.; Brulliet, S.; Brusch, C.V.; Caldwell, A.B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabre, C.; Ferrari, E.
Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizi, A.; Gall
lech, J.; Harwood, C.R.; Henauf, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidis, A.; Lardinois,
A;Authors: Lamber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y, M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel
Rieger, M.; Rivolta, C.; Roche, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A;Authors: Schlecht, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Ser
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Toigoni, A.; Tosato, V.; Uchiyama,
T.; Wintere, P.; Wipac, A.; Yamamoto, H.; Yamano, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A;Authors: Yoshikawa, H.F.; Zunsstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: H69834
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-108 <KIN>
A;Cross-references: GB:Z99109; GB:AL009126; NID:92633260; PIDN:CAB12900.1; PID:el183062;
A;Experimental source: strain 168

C;GeneticS:
A;Gene: yhjQ

Query Match 8.8%; Score 80; DB 2; Length 108;
Best Local Similarity 23.6%; Pred. No. 3.5;
Matches 25; Conservative 9; Mismatches 26; Indels 46; Gaps 5;

Qy 37 EOYMPPLGTGMSCKTICN-----QSORTCA----- 63
Db 2 EOYSACIEACIDCKACNHCFTKCLBSVOHLSGCRRLRRECDTALAVKAMQTSNP 61

Qy 64 -----AFCRSL--SCRKQKRF-YHLRDCISCAISCGQHKKQ 100
Db 62 FMKEICACADICEACGTEGKHDDH----CQACAKACFTCAEQC 103

RESULT 15
125169
hypothetical protein T23F1.6 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T25169

R;Wilkinson, U.
submitted to the EMBL Data Library, October 1996
A;Reference number: 219990
A;Accession: T25169

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-330 <WIL>
A;Cross-references: EMBL:Z81129; PIDN:CAB03405.1; GSPDB:GN00023; CESP:T23F1.6

A;Experimental source: clone T23F1
C;GeneticS:
A;Gene: CESP:T23F1.6
A;Map position: 5
A;introns: 16/3
C;Superfamily: gliadin

Query Match 8.8%; Score 80; DB 2; Length 330;
Best Local Similarity 24.6%; Pred. No. 9.4;
Matches 33; Conservative 14; Mismatches 55; Indels 32; Gaps 8;

Qy 33 SCPEBQWDPPLGTGM-----SKTTIC-----NHOSQRTCAAFCSLSCKRKG--KTYD 80
Db 58 SCASSQYQQLQTSQCMPCAGQSCSQGCSQNTNTQCPQCGQSCGSCNPMSTPPIASQ 117

Qy 81 HILRDCIS-CAISCGQ--PRQCAVFCENKLRSPVNLPELRQSGE---VENNSD-- 131
Db 118 SCLPCEKCRKMQCQCTQQTQADCCCPICQDCC-----QDCGSGTGMMYNNQDPY 166

Oy 132 NSGRYQGLEHRSSE 145
| : | : | :
Db 167 NQWQYGGYNQOGNQ 180

Search completed: February 4, 2003, 12:59:52
Job time : 26.4899 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 4, 2003, 12:56:41 ; Search time 7.54251 Seconds
(without alignments)
315.977 Million cell updates/sec

Title: US-09-854-864-13

Perfect score: 498
Sequence: 1 CSONEHYPSILHACIPQCLR.....SEYPSILHACPRATCPYC 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
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5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	93	18.7	166	2	US-08-810-572A-6
2	93	18.7	166	4	US-09-290-333-6
3	93	18.7	293	4	US-08-810-572A-2
4	93	18.7	293	4	US-09-290-333-2
5	82	16.5	508	4	US-09-019-095A-8
6	82	16.5	521	4	US-09-019-095A-22
7	82	16.5	526	4	US-09-019-095A-2
8	80	16.1	3075	2	US-08-460-309-5
9	80	16.1	3075	2	US-08-125-077-5
10	80	16.1	5405	4	US-08-718-388-9
11	79	15.9	320	4	US-09-183-861-22
12	79	15.9	320	4	US-09-183-861-55
13	79	15.9	320	4	US-09-022-765-22
14	79	15.9	320	4	US-09-022-765-22
15	79	15.9	545	4	US-09-022-765-55
16	78	15.7	109	2	US-08-527-044-2
17	78	15.7	109	2	US-09-013-780-2
18	77.5	15.6	139	3	US-08-965-903B-20
19	77.5	15.6	139	4	US-09-370-398-4
20	76.5	15.4	2414	1	US-08-227-536-2
21	76.5	15.4	2414	1	PCT-US95-04682-2
22	76	15.3	2441	1	US-08-194-468-2
23	76	15.3	2441	3	US-08-961-739-2
24	76	15.3	2441	4	US-09-514-247A-8
25	76	15.3	2442	4	US-09-514-247A-10
26	75.5	15.2	156	3	US-08-600-982-30
27	75.5	15.2	156	5	PCT-US94-10261A-30

28	75.5	15.2	1713	3	US-08-600-982-24	Sequence 24, Appl
29	75.5	15.2	1713	5	PCT-US94-10261A-24	Sequence 24, Appl
30	75	15.1	219	1	US-08-152-019A-31	Sequence 31, Appl
31	75	15.1	219	2	US-08-460-309-18	Sequence 18, Appl
32	75	15.1	219	2	US-08-125-077-18	Sequence 18, Appl
33	75	15.1	430	3	US-08-997-897-2	Sequence 2, Appl
34	75	15.1	430	4	US-09-156-836B-2	Sequence 2, Appl
35	73.5	14.8	435	4	US-09-561-989-10	Sequence 10, Appl
36	73	14.7	689	4	US-09-177-249-2	Sequence 2, Appl
37	73	14.7	689	4	US-09-061-769A-2	Sequence 2, Appl
38	72.5	14.6	969	2	US-08-284-941-2	Sequence 2, Appl
39	72.5	14.6	969	2	US-08-447-642-2	Sequence 2, Appl
40	72.5	14.6	969	4	US-09-236-503-2	Sequence 2, Appl
41	72.5	14.6	969	5	PCT-US93-02147A-2	Sequence 2, Appl
42	72	14.5	275	1	US-08-312-870-7	Sequence 7, Appl
43	72	14.5	366	4	US-08-857-076-103	Sequence 103, App
44	72	14.5	446	1	US-08-307-444A-5	Sequence 5, Appl
45	72	14.5	446	1	US-08-587-389-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-810-572A-6
Sequence 6, Application US/08810572A
Patent No. 5969102
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
APPLICANT: von Bulow, Goetz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
TITLE OF INVENTION: THEROF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,572A
FILING DATE: 28-FEB-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-810-572A-6
Query Match 18.7%; Score 93; DB 2; Length 166;
Best Local Similarity 28.4%; Pred. No. 0.037;


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US-09-019-095A-8
: ORGANISM: Murine
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Query Match 16.5%; Score 82; DB 4; Length 508;
Best Local Similarity 35.8%; Pred. No. 1.2;
Matches 19; Conservative 8; Mismatches 18; Indels 8; Gaps 2;

Oy 19 LRCSSNTPPLTCQRYCCYFDSLHLHACPLCRSPPTQCYCCFHSYFDSLHA 71
Db 55 LQCLHTHTPL-----ADYMLSGEHSQTC--CSPEGCKLCAMEALVTSLSLHS 99

RESULT 6
US-09-019-095A-22
: Sequence 22, Application US/09019095A
: Patent No. 6287858
: GENERAL INFORMATION:
: APPLICANT: D'Andrea, Alan D.
: TITLE OF INVENTION: Deubiquitinating Enzymes That Regulate
: TITLE OF INVENTION: Cell Growth
: FILE REFERENCE: DPCI-435D2A2
: CURRENT APPLICATION NUMBER: US/09/019,095A
: CURRENT FILING DATE: 1998-02-05
: PRIOR APPLICATION NUMBER: PCT/US96/12884
: PRIOR FILING DATE: 1996-08-07
: PRIOR APPLICATION NUMBER: US 60/002,066
: PRIOR FILING DATE: 1995-08-09
: PRIOR APPLICATION NUMBER: US 60/019,787
: PRIOR FILING DATE: 1996-06-14
: NUMBER OF SEQ ID NOS: 51
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 22
: LENGTH: 521
: TYPE: PRT
: ORGANISM: Murine
US-09-019-095A-22

Query Match 16.5%; Score 82; DB 4; Length 521;
Best Local Similarity 35.8%; Pred. No. 1.2;
Matches 19; Conservative 8; Mismatches 18; Indels 8; Gaps 2;

Oy 19 LRCSSNTPPLTCQRYCCYFDSLHLHACPLCRSPPTQCYCCFHSYFDSLHA 71
Db 61 LQCLHTHTPL-----ADYMLSGEHSQTC--CSPEGCKLCAMEALVTSLSLHS 105

RESULT 7
US-09-019-095A-2
: Sequence 2, Application US/09019095A
: Patent No. 6287858
: GENERAL INFORMATION:
: APPLICANT: D'Andrea, Alan D.
: TITLE OF INVENTION: Deubiquitinating Enzymes That Regulate
: TITLE OF INVENTION: Cell Growth
: FILE REFERENCE: DPCI-435D2A2
: CURRENT APPLICATION NUMBER: US/09/019,095A
: CURRENT FILING DATE: 1998-02-05
: PRIOR APPLICATION NUMBER: PCT/US96/12884
: PRIOR FILING DATE: 1996-08-07
: PRIOR APPLICATION NUMBER: US 60/002,066
: PRIOR FILING DATE: 1995-08-09
: PRIOR APPLICATION NUMBER: US 60/019,787
: PRIOR FILING DATE: 1996-06-14
: NUMBER OF SEQ ID NOS: 51
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 526
: TYPE: PRT
: ORGANISM: Murine
US-09-019-095A-2

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Query Match 16.5%; Score 82; DB 4; Length 526;
Best Local Similarity 35.8%; Pred. No. 1.2;
Matches 19; Conservative 8; Mismatches 18; Indels 8; Gaps 2;

QY 19 LRCSNTPPLTCRCYCEYFDSLHACPCRCSPPTCYCCPFSEYFDSLHA 71
DB 66 LQCLTHPLP-----ADYMLSGEHSQTC--CSPECKLCAEMALVTQSILHS 110

RESULT 8

US-08-460-309-5
; Sequence 5, Application US/08460309
; Patent No. 5837496
; GENERAL INFORMATION:
; APPLICANT: Engvall, Eva
; APPLICANT: Leivo, Ilmo
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; TITLE OF INVENTION: Fragments and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,309
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,077
; FILING DATE: 22-SEP-1993
; APPLICATION NUMBER: US PCT/US 94/10730
; FILING DATE: 21-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/472,319
; FILING DATE: 30-JAN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/919,951
; FILING DATE: 27-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9721
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3075 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-460-309-5

Query Match 16.1%; Score 80; DB 2; Length 3075;

Best Local Similarity 23.4%; Pred. No. 10;
Matches 29; Conservative 10; Mismatches 37; Indels 48; Gaps 8;

QY 1 CSQNEFYFDSL--HACIPCO-----LRCSNTPPLTCRCYCC-- 36
DB 831 CADGYGNPTVPGESCVPCDCSGNVDPSEAGHCDSTVTECLKLGANTDGAHCR--CADGF 889
QY 37 YPDSL-----LHACPC-----LRCSNTPPLTCRCYCC-- 73
DB 890 YGDAYTAKKRCRACGCHVAGSHSAVCHLETGLCDCKPNVTGQCCDGLHGYGLDSGHCR 949
QY 74 PATC 77

DB 950 PCNC 953

RESULT 9

US-08-125-077-5
; Sequence 5, Application US/08125077
; Patent No. 5872231
; Patent No. 5872231 5840863
; GENERAL INFORMATION:
; APPLICANT: Engvall, Eva
; APPLICANT: Leivo, Ilmo
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; TITLE OF INVENTION: Fragments and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/125,077
; FILING DATE: 22-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US 94/10730
; FILING DATE: 21-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/472,319
; FILING DATE: 30-JAN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/919,951
; FILING DATE: 27-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9721
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3075 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-125-077-5

Query Match 16.1%; Score 80; DB 2; Length 3075;

Best Local Similarity 23.4%; Pred. No. 10;
Matches 29; Conservative 10; Mismatches 37; Indels 48; Gaps 8;

QY 1 CSQNEFYFDSL--HACIPCO-----LRCSNTPPLTCRCYCC-- 36
DB 831 CADGYGNPTVPGESCVPCDCSGNVDPSEAGHCDSTVTECLKLGANTDGAHCR--CADGF 889
QY 37 YPDSL-----LHACPC-----LRCSNTPPLTCRCYCC-- 73
DB 890 YGDAYTAKKRCRACGCHVAGSHSAVCHLETGLCDCKPNVTGQCCDGLHGYGLDSGHCR 949
QY 74 PATC 77
DB 950 PCNC 953

RESULT 10
US-08-718-388-9

Sequence 9, Application US/08718388
Patent No. 6271362
GENERAL INFORMATION
APPLICANT: MORIKAWA, MINORU
APPLICANT: HARADA, NAOKI
TITLE OF INVENTION: GENE ENCODING IGG Fc REGION-BINDING
PROTEIN
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,388
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 0230-111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 5405 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-718-388-9

Query Match 16.1%; Score 80; DB 4; Length 5405;
Best Local Similarity 25.4%; Pred. No. 17;
Matches 29; Conservative 12; Mismatches 25; Indels 48; Gaps 10;

Qy 1 CSQNEFYPSLHACT-PCQLRCSNTPPLTCQYCCCEYFDSLHACPC-----LRCS 51
Db 2733 CPQNGHYE---LCADTCSLGSALSAPLQCCPDGCAE-----GQCDSGRLYNQACV 2781

Qy 52 PTCQYC-CFHS-BYFD---SLI-----HACPPA-TQCP 79
Db 2782 P--100CGCYHNGAYEPEQTVLIDNCRQOCTCHAGKVVVCOEHSCKPQVCOP 2833

RESULT 11
US-09-183-861-22
Sequence 22, Application US/09183861
Patent No. 6365165
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yashir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/183,861
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/022,765
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David U.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-183-861-22

Query Match 15.9%; Score 79; DB 4; Length 320;
Best Local Similarity 27.5%; Pred. No. 15;
Matches 25; Conservative 11; Mismatches 23; Indels 32; Gaps 7;

Qy 13 ACIPQ-----LRCSN---TPPLTCQYCCCEYFDSLHACPLRCSPT- 54
Db 105 ACVRCQENCFSCDSKANKCQACAPNYVLTPLTCSPVAC---NIH---CMQCDPQT 157

Qy 55 --COYCC--FHSEYFDSLH---ACPPATCQ 78
Db 158 SRCQCVSPYVVDYDGLCRISDACSPVNC 183

RESULT 12
US-09-183-861-55
Sequence 55, Application US/09183861
Patent No. 6365165
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yashir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/183,861
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/022,765
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David U.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-183-861-55

Query Match 15.9%; Score 79; DB 4; Length 320;
Best Local Similarity 27.5%; Pred. No. 1.5;
Matches 25; Conservative 11; Mismatches 23; Indels 32; Gaps 7;

QY 13 ACIPQ-----LRSSN---TPPLTCQRYCCEYFDSLHLACPLRCSPPT- 54
DB 105 ACVRCQEPNCFSCDSANKCTQCAPNYLTPLLTCSPVAC---NIEH---CMQCDPQTP 157
QY 55 --COYCC--FHSEYFDSLH---ACPPATCQ 78
DB 158 SRCQECVSPYVDSYDGLCRSLDACSVPNCK 188

RESULT 13
US-09-022-765-22
Sequence 22, Application US/09022765
Patent No. 6375955
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, David C.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSER: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,765
FILING DATE: 12-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-765-22

Query Match 15.9%; Score 79; DB 4; Length 320;
Best Local Similarity 27.5%; Pred. No. 1.5;
Matches 25; Conservative 11; Mismatches 23; Indels 32; Gaps 7;

QY 13 ACIPQ-----LRSSN---TPPLTCQRYCCEYFDSLHLACPLRCSPPT- 54
DB 105 ACVRCQEPNCFSCDSANKCTQCAPNYLTPLLTCSPVAC---NIEH---CMQCDPQTP 157
QY 55 --COYCC--FHSEYFDSLH---ACPPATCQ 78
DB 158 SRCQECVSPYVDSYDGLCRSLDACSVPNCK 188

RESULT 14
US-09-022-765-55
Sequence 55, Application US/09022765
Patent No. 6375955
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, David C.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSER: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,765
FILING DATE: 12-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-022-765-55

Query Match 15.9%; Score 79; DB 4; Length 320;
Best Local Similarity 27.5%; Pred. No. 1.5;
Matches 25; Conservative 11; Mismatches 23; Indels 32; Gaps 7;

QY 13 ACIPQ-----LRSSN---TPPLTCQRYCCEYFDSLHLACPLRCSPPT- 54
DB 105 ACVRCQEPNCFSCDSANKCTQCAPNYLTPLLTCSPVAC---NIEH---CMQCDPQTP 157
QY 55 --COYCC--FHSEYFDSLH---ACPPATCQ 78
DB 158 SRCQECVSPYVDSYDGLCRSLDACSVPNCK 188

RESULT 15
US-09-019-095A-38
Sequence 38, Application US/09019095A
Patent No. 6287858
GENERAL INFORMATION:
APPLICANT: D'Andrea, Alan D.

; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: Deubiquitinating Enzymes That Regulate
; TITLE OF INVENTION: Cell Growth
; FILE REFERENCE: DFCL-435P2A2
; CURRENT APPLICATION NUMBER: US/09/019,095A
; CURRENT FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: PCT/US96/12884
; PRIOR FILING DATE: 1996-08-07
; PRIOR APPLICATION NUMBER: US 60/002,066
; PRIOR FILING DATE: 1995-08-09
; PRIOR APPLICATION NUMBER: US 60/019,787
; PRIOR FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 545
; TYPE: PRT
; ORGANISM: murine
US-09-019-095A-38

Query Match 15.9%; Score 79; DB 4; Length 545;
Best Local Similarity 34.0%; Pred. No. 2.4;
Matches 18; Conservative 9; Mismatches 18; Indels 8; Gaps 2;

QY 19 LRCSNTPTPTQRYCEYFDLSLHACPLRCSPPTQYCCFHSEYFDLSLHA 71
Db 66 LQCLTHTPPL-----ADYMLSQEYSQTC--CSPEGCKWKAMEAHVTSLSLHS 110

Search completed: February 4, 2003, 13:00:15
Job time: 10.5425 secs

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OM protein - protein search, using SW model

Run on: February 4, 2003, 12:59:16 ; Search time 5.24696 Seconds
(without alignments)
342.239 Million cell updates/sec

Title: US-09-854-864-13

Perfect score: 498
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 129505 seqs, 22169297 residues

Total number of hits satisfying chosen parameters: 129505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep:.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	230.5	46.3	207	9 US-10-077-438-3	Sequence 3, Appl
3	230.5	46.3	207	9 US-10-077-137-3	Sequence 3, Appl
4	201.5	40.5	283	10 US-09-854-864-9	Sequence 7, Appl
5	201	40.4	34	10 US-09-854-864-7	Sequence 7, Appl
6	201	40.4	51	10 US-09-854-864-6	Sequence 6, Appl
7	201	40.4	58	10 US-09-854-864-21	Sequence 2, Appl
8	201	40.4	181	10 US-09-854-864-5	Sequence 5, Appl
9	201	40.4	184	9 US-10-077-438-1	Sequence 1, Appl
10	201	40.4	184	9 US-10-077-438-7	Sequence 7, Appl
11	201	40.4	184	9 US-10-077-137-1	Sequence 1, Appl
12	201	40.4	184	9 US-10-077-137-7	Sequence 7, Appl
13	201	40.4	184	9 US-10-068-725-2	Sequence 2, Appl
14	153	30.7	117	10 US-09-854-864-12	Sequence 12, Appl
15	139.5	28.0	281	10 US-09-854-864-10	Sequence 10, Appl
16	136	27.3	185	10 US-09-854-864-11	Sequence 11, Appl
17	105	21.1	67	10 US-09-854-864-16	Sequence 16, Appl
18	93	18.7	166	10 US-09-854-864-15	Sequence 15, Appl
19	93	18.7	291	9 US-09-779-050A-43	Sequence 43, Appl

20	93	18.7	293	9 US-09-779-050A-42	Sequence 42, Appl
21	93	18.7	293	9 US-10-084-971-2	Sequence 2, Appl
22	93	18.7	293	9 US-10-068-725-4	Sequence 4, Appl
23	93	18.7	293	9 US-09-302-863-2	Sequence 2, Appl
24	93	18.7	293	10 US-09-879-919-22	Sequence 22, Appl
25	93	18.7	293	10 US-09-854-864-14	Sequence 14, Appl
26	93	18.7	293	10 US-09-961-376-2	Sequence 2, Appl
27	93	18.7	293	10 US-09-854-864-18	Sequence 18, Appl
28	91.5	18.4	231	10 US-09-864-761-37946	Sequence 37946, A
29	89.5	18.0	134	10 US-09-864-761-39564	Sequence 39564, A
30	84.5	17.0	270	10 US-09-764-855-145	Sequence 145, App
31	83	16.7	293	10 US-09-864-761-46675	Sequence 46675, A
32	82	16.5	230	10 US-09-874-062-3	Sequence 3, Appl
33	81	16.3	241	9 US-10-084-994-8	Sequence 8, Appl
34	81	16.3	1587	10 US-09-845-583-10	Sequence 10, Appl
35	80.5	16.2	85	10 US-09-864-761-39864	Sequence 39864, A
36	80.5	16.2	1798	10 US-09-938-275-9	Sequence 5, Appl
37	80	16.1	3075	10 US-09-938-275-5	Sequence 5, Appl
38	80	16.1	5405	9 US-10-025-380-1116	Sequence 1116, Ap
39	80	16.1	5405	10 US-09-922-217-1116	Sequence 1116, Ap
40	79	15.9	59	10 US-09-854-864-20	Sequence 20, Appl
41	79	15.9	320	9 US-09-991-496-22	Sequence 22, Appl
42	79	15.9	320	9 US-09-991-496-55	Sequence 55, Appl
43	79	15.9	320	10 US-09-874-923-22	Sequence 22, Appl
44	79	15.9	320	10 US-09-874-923-55	Sequence 55, Appl
45	79	15.9	709	9 US-09-991-496-121	Sequence 121, App

ALIGNMENTS

```
RESULT 1
US-09-854-864-13
; Sequence 13, Application US/09854864
; Patent No. US20020081286A1
; GENERAL INFORMATION:
; APPLICANT: THERIL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AP-3, AND TACI
; FILE REFERENCE: A-6868
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
; US-09-854-864-13

Query Match      100.0%; Score 498; DB 10; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.6e-35;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CSONEFDSLHACIPQCLRCSNTPTLCORCCYFDSLHACPCLRCSPPTCYCCF 60
DB      1 CSONEFDSLHACIPQCLRCSNTPTLCORCCYFDSLHACPCLRCSPPTCYCCF 60
QY      61 HSEYFDSLHACPPATCPYC 81
DB      61 HSEYFDSLHACPPATCPYC 81

RESULT 2
US-10-077-438-3
; Sequence 3, Application US/10077438
; Patent No. US20020165156A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-3

Query Match          46.3%; Score 230.5; DB 9; Length 207;
Best Local Similarity 57.8%; Pred. No. 6,4e-13;
Matches 48; Conservative 0; Mismatches 4; Indels 31; Gaps 4;
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Qy 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYCCYFDSLHAC-PC-LRCSPTQCYC 58
    |||||
Db 46 CSQNEYPDSLHACIPCOLRCSSNTPPLTC-----LHACIPCOLRCSSNT----- 90
Qy 59 CPHSEYFDSLHACPPATQCPYC 81
    |||||
Db 91 -----PPLTCQRYC 99
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RESULT 3
US-10-077-137-3
; Sequence 3, Application US/10077137
; Patent No. US2002012674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-3
```

Query Match 46.3%; Score 230.5; DB 9; Length 207;

```

Best Local Similarity 57.8%; Pred. No. 6,4e-13;
Matches 48; Conservative 0; Mismatches 4; Indels 31; Gaps 4;

Qy 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYCCYFDSLHAC-PC-LRCSPTQCYC 58
    |||||
Db 46 CSQNEYPDSLHACIPCOLRCSSNTPPLTC-----LHACIPCOLRCSSNT----- 90
Qy 59 CPHSEYFDSLHACPPATQCPYC 81
    |||||
Db 91 -----PPLTCQRYC 99
```

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RESULT 4
US-09-854-864-9
; Sequence 9, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-9

Query Match          40.5%; Score 201.5; DB 10; Length 283;
Best Local Similarity 60.6%; Pred. No. 2.1e-10;
Matches 40; Conservative 2; Mismatches 9; Indels 15; Gaps 3;
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Qy 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC-CEYFDSL-----LHAPRC 47
    |||||
Db 5 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYCNASTVNSKGTNAGGGGDKTHTCP- 63
Qy 48 IRCSP 53
    |||
Db 64 -PCPAP 68
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RESULT 5
US-09-854-864-7
; Sequence 7, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-7
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Query Match 40.4%; Score 201; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 4e-11;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34

RESULT 6

US-09-854-864-6
; Sequence 6, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-6

Query Match 40.4%; Score 201; DB 10; Length 51;
Best Local Similarity 100.0%; Pred. No. 5.6e-11;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 5 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 38

RESULT 7

US-09-854-864-21
; Sequence 21, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-21

Query Match 40.4%; Score 201; DB 10; Length 58;
Best Local Similarity 100.0%; Pred. No. 6.3e-11;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34

RESULT 8
US-09-854-864-5
; Sequence 5, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-5

Query Match 40.4%; Score 201; DB 10; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 5 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 38

RESULT 9

US-10-077-438-1
; Sequence 1, Application US/10077438
; Patent No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Teschop, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech Rad S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-1

Query Match 40.4%; Score 201; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34

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Db      8 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 10
US-10-077-438-7
; Sequence 7, Application US/10077438
; Patent No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Teschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-7

Query Match
Best Local Similarity 100.0%; Score 201; DB 9; Length 184;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db      8 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 11
US-10-077-137-1
; Sequence 1, Application US/10077137
; Patent No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Teschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
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; ORGANISM: homo sapien
US-10-077-137-1

Query Match
Best Local Similarity 100.0%; Score 201; DB 9; Length 184;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db      8 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 12
US-10-077-137-7
; Sequence 7, Application US/10077137
; Patent No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Teschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-7

Query Match
Best Local Similarity 100.0%; Score 201; DB 9; Length 184;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db      8 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 13
US-10-068-725-2
; Sequence 2, Application US/10068725
; Publication No. US20030012783A1
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne
; TITLE OF INVENTION: Antibodies That Bind Both BCMA and TACI
; FILE REFERENCE: 01-04
; CURRENT APPLICATION NUMBER: US/10/068,725
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/270,274
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/283,447
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-068-725-2

Query Match 40.4%; Score 201; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34
DB 8 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 14
US-09-854-864-12

; Sequence 12, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: human-murine Consensus
US-09-854-864-12

Query Match 30.7%; Score 153; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 CEYFDSLHACPCLRCSPTCQYC 58
DB 4 CEYFDSLHACPCLRCSPTCQYC 27

RESULT 15
US-09-854-864-10

; Sequence 10, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10

Query Match 28.0%; Score 139.5; DB 10; Length 281;
Best Local Similarity 45.5%; Pred. No. 3.1e-05;
Matches 30; Conservative 3; Mismatches 16; Indels 17; Gaps 3;

QY 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYCEYFDSLHACPC-----HACPC 47

DB 5 CFHSEYFDSLHACPCHLRCSN--PPATCOPYCDPSVTSVKSGYTGAGGGGDKHTTCP- 61
QY 48 IRCSP 53
DB 62 -PCPAP 66

Search completed: February 4, 2003, 13:05:57
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OM protein - protein search, using sw model

Run on: February 4, 2003, 12:52:56 ; Search time 20.6599 Seconds
(without alignments)
522.427 Million cell updates/sec

Title: US-09-854-864-13

Perfect score: 458
Sequence: 1 CSQNPYPSLLHACIPQLR.....SEYPSLLHACPPATCPYC 81

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Post-processing: Minimum Match 0%
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8: /SIDP2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SIDP2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SIDP2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SIDP2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SIDP2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SIDP2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SIDP2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SIDP2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
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19: /SIDP2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDP2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDP2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDP2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDP2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	205	41.2	302	22	AAE00507
2	205	41.2	302	22	AAE00507
3	201.5	40.5	283	22	AAE06099
4	201	40.4	34	23	AAE15488
5	201	40.4	51	23	AAE15485
6	201	40.4	58	23	AAE15501
7	201	40.4	181	23	AAE15484
8	201	40.4	184	21	AAE08843
9	201	40.4	184	21	AAE194001
10	201	40.4	184	22	AAE09241

11	201	40.4	184	22	AAE00506	Human B cell matur
12	201	40.4	184	22	AAE06098	Human BAF receptor
13	201	40.4	184	22	AAE17979	Human B cell matur
14	201	40.4	184	23	AAE01487	Human BCFM receptor
15	159.5	32.0	157	22	AAE07000	Human BAF receptor
16	153	30.7	24	23	AAE15482	Human-murine BCMA
17	153	30.7	117	23	AAE15491	Human-murine B cell
18	139.5	28.0	281	23	AAE15489	Mouse BCMA-human 1
19	136	27.3	185	21	AAE08844	Amino acid sequenc
20	136	27.3	185	22	AAE1980	Murine B cell matur
21	136	27.3	185	23	AAE15480	Mouse B cell matur
22	100.5	20.2	334	23	AAE01413	Protein of hTACI (
23	100.5	20.2	366	23	AAE01413	Protein of hTACI (
24	98	19.7	249	21	AAE194006	A murine znf4, a
25	96.5	19.4	301	22	AAE19986	Human protein SEQ
26	95	19.1	256	22	AAE08337	Novel human diagno
27	95	19.1	351	19	AAE23698	Novel human diagno
28	93	18.7	166	23	AAE15485	Human lymphocyte s
29	93	18.7	166	23	AAE15494	Human TACI splice
30	93	18.7	265	22	AAE09244	Human TACI extrace
31	93	18.7	291	23	AAE10949	Human AGP-3 recept
32	93	18.7	293	19	AAE15783	Human lymphocyte s
33	93	18.7	293	21	AAE16312	Human neutrophil-a
34	93	18.7	293	21	AAE194000	A transmembrane ac
35	93	18.7	293	23	AAE09240	Human TACI protein
36	93	18.7	293	22	AAE19114	Human tumour necro
37	93	18.7	293	23	AAE19512	Human TACI-IgG Fc
38	93	18.7	293	23	AAE1488	Human TACI recepto
39	93	18.7	293	23	AAE014130	Human transmembran
40	93	18.7	293	23	AAE15408	Tumour necrosis fa
41	93	18.7	293	23	AAE15493	Human transmembran
42	93	18.7	293	23	AAE19900	Human AGP-3 relate
43	93	18.7	312	23	AAE014135	Protein of N-termi
44	93	18.7	397	23	AAE15498	Human TACI-immuno
45	93	18.7	404	23	AAE014136	Protein of a compl

ALIGNMENTS

RESULT 1	AAE00507	AAE00507 standard; Protein; 302 AA.
AC	AAE00507;	
DT	31-JUL-2001	(first entry)
DE	Human BCMA-Immunoglobulin G Fc region fusion construct.	
XX	Human: A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;	
XX	gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;	
XX	carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;	
XX	systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;	
XX	B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;	
XX	organ transplantation; HIV; human immunodeficiency virus; TGF; murine;	
XX	tumour necrosis factor; B cell maturation protein; BCMA; fusion protein;	
XX	immunoglobulin G; IgG; Fc region.	
OS	Chimeric - Homo sapiens.	
OS	Chimeric - Mus sp.	
XX		
Key	Location/Qualifiers	
FT	1..22	/label= Signal_peptide
FT	/note= "Derived from murine Ig kappa sequence"	
FT	23..302	/label= Mature_human_BCMA_IgG_Fc_fusion_protein
FT	23..75	/note= "Derived from human BCMA protein"
FT	76..302	/note= "Derived from human IgG Fc region"
FT	24..302	
FT	Domain	

```

FT      /label= Cysteine-rich domain
FT      /note= "Derived from human BCMA"
XX
XX      WO200124811-A1.
XX
XX      12-APR-2001.
XX
XX      05-OCT-2000; 2000WO-US27579.
XX
XX      06-OCT-1999; 99US-0157933.
XX      PR      11-FEB-2000; 2000US-0181807.
XX      PR      30-JUN-2000; 2000US-0215686.
XX
XX      (BIOJ ) BIOGEN INC.
XX      (APOT-) APOTEC R & D SA.
XX
XX      Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;
XX      WPI, 2001-266242/27.
XX      DR      N-PSDB; AAD03847.
XX
XX      Treating a mammal for a condition associated with undesired cell
XX      PT      proliferation such as cancer or carcinoma, comprises administering a
XX      PT      composition comprising A Proliferation Inducing Ligand Receptor
XX      PT      (APRIL-R) antagonist
XX
XX      Example 1; Fig 3B; 855p; English.
XX
XX      The invention relates to a method of treating a mammal for a condition
XX      CC      associated with undesired cell proliferation such as cancer or
XX      CC      carcinoma. The method involves administering a composition comprising
XX      CC      A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as
XX      CC      B cell maturation protein (BCM or BCMA) antagonist that antagonises the
XX      CC      interaction between APRIL and its cognate receptor(s) . This method is
XX      CC      useful for treating undesired cell proliferation such as cancer or
XX      CC      carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
XX      CC      prostate carcinoma, and other carcinomas whose proliferation is modulated
XX      CC      by APRIL. It is also useful for treating autoimmune diseases (Grave's
XX      CC      disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
XX      CC      diseases, renal disorders, B-cell lympho-proliferative disorders,
XX      CC      immunosuppressive diseases, organ transplantation, inflammation and
XX      CC      human immunodeficiency virus (HIV), and for treating, suppressing or
XX      CC      altering an immune response involving a signalling pathway between
XX      CC      APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy.
XX      CC      The present sequence is a fusion construct containing human APRIL-R
XX      CC      also referred as BCMA or BCM protein, Fc region of human immunoglobulin
XX      CC      G (IgG) and a signal sequence from murine Ig kappa cDNA.
XX
XX      Sequence 302 AA;
XX
XX      Query Match 41.2%; Score 205; DB 22; Length 302;
XX      Best Local Similarity 67.8%; Pred. No. 2,3e-10;
XX      Matches 40; Conservative 2; Mismatches 9; Indels 8; Gaps 3
XX
XX      1 CSQNEYFDSLHACIPQQLRCSSNTPPTLCQRYC-CERYFDSL-----LHACPCLRCSP 53
XX      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX      Db 31 CSQNEYFDSLHACIPQQLRCSSNTPPTLCQRYC-CERYFDSL-----LHACPCLRCSP 53
XX
XX      AAB60699 standard; Protein; 302 AA.
XX
XX      AAB60699;
XX
XX      22-MAY-2001 (first entry)
XX
XX      Mouse Igg signal/human BAPF-R/human Igg Fc fusion protein, BAPF-R-Fc.
XX
XX      Human BAPF-R; BAPF receptor; TNF family; immunoregulatory agent;
XX      KW      immune-related disorder; B-cell growth inhibitor;
XX      *      B-cell maturation inhibitor; immunoglobulin production inhibitor;
XX      KW      autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;

```

renal disorder; immunosuppressive disorder; HIV infection;
organ transplant; antinflammatory; systemic lupus erythematosus;
autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
lymphoma; gene therapy; cancer; tumour; IgG Fc; fusion construct.
Chimeric - Homo sapiens.
Chimeric - Mus sp.
WO200112812-A2.
22-FEB-2001.
16-AUG-2000; 2000WO-US22507.
17-AUG-1999; 99US-0149378.
11-FEB-2000; 2000US-0181684.
18-FEB-2000; 2000US-0183536.
(BIOJ) BIOGEN INC.
(APOT-) APOTEC R & D SA.
Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;
Thompson J;
WPI; 2001-202866/20.
N-PSDB; AAF59999.
Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
lympho-proliferative disorder by administering BAF-R-receptor
polypeptide, chimeric molecule comprising receptor or anti-BAF-R
antibody homolog -
Example 4; Fig 2; 59pp; English.
The invention relates to the use of a BAF-R receptor (BAF-R, also known
as BCM) protein, or a BAF-R fusion protein as an agent for the
treatment of a variety of immune-related disorders. BAF-R is a member of
the TNF (tumour necrosis factor) family, acting as an immunoregulatory
agent, and also plays a role in the development of hypertension and
related disorders. BAF-R, fusion proteins containing it, and BAF-R-
specific antibodies can be used for inhibiting B-cell growth, dendritic
cell-induced B-cell growth and maturation, and immunoglobulin production,
in the treatment of autoimmune disorders, B-cell lymphoproliferative
disorders, hypertension and renal disorders. The BAF-R proteins may also
be used in the treatment of immunosuppressive disorders and HIV
infection, and in patients undergoing organ transplantation. The BAF-R
proteins or BAF-R specific antibodies may be used for treating,
suppressing or altering an immune response involving a signalling pathway
between BAF-R and BAF, thereby inhibiting inflammation. Since BAF-R
inhibits B-cell growth and maturation it is useful for treating diseases
such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
human BAF-R may be used in gene therapy to treat tumours, lymphomas,
autoimmune disorders and inherited B-cell-associated disorders. The
present sequence represents the BAF-R fusion protein BAF-R-Fc,
comprising a mouse IgG-kappa signal sequence, residues 1-153
of human BAF-R and a human IgG Fc sequence.

Query Match 41.2% Score 205; DB 22; Length 302;
Best Local Similarity 67.8% Pred. No. 2.3e-10;
Matches 40; Conservative 2; Mismatches 9; Indels 8; Gaps 3

1 CSQNYFDSLHACTPCQLRCSNTPPTTCQRYC-CEYFDSL-----LHACPLRCSPP 53
Db 31 CSQNYFDSLHACTPCQLRCSNTPPTTCQRYCNASTYNSYKGVDKHTCC--PCPAP 87

RESULT 3
AAE15488

ID AAE15488 standard; Protein; 283 AA.
 AC AAE15488;
 XX
 XX
 DT 12-MAR-2002 (first entry)
 DE Human BCMA-immunoglobulin Fc region fusion protein.
 XX
 KW Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytosolic; B cell maturation protein; BCMA; tumor necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis; fusion protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200187979-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 14-MAY-2001; 2001WO-US15567.
 XX
 PR 12-MAY-2000; 2000US-204039P.
 PR 27-JUN-2000; 2000US-214591P.
 PR 14-MAY-2001; 2001US-0214591.
 PA (AMGE-) AMGEN INC.
 XX
 PI The111 LE, Yu G;
 XX
 DR WPI; 2002-066686/09.
 XX
 XX Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand -
 XX
 PS Disclosure; Fig 10B; 94pp; English.
 XX
 CC The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA protein-immunoglobulin Fc region fusion protein.
 XX
 SQ Sequence 283 AA;
 Query Match 40.5%; Score 201.5; DB 23; Length 283;
 Best Local Similarity 60.6%; Pred. No. 4.4e-10;
 Matches 40; Conservative 2; Mismatches 9; Indels 15; Gaps 3;
 QY 1 CSQNYFSPSLHAGIPCOLRGSSNTPPLTCORYC-CEYFDSL-----LHAGPC 47
 DB 5 CSQNYFSPSLHAGIPCOLRGSSNTPPLTCORYCNASTVYKGNAGGGGDKTHTCP- 63
 QY 48 LRCSP 53

DB 64 -PCPAP 68
 RESULT 4
 ID AAE15486
 AC AAE15486 standard; peptide; 34 AA.
 XX
 XX
 DT 12-MAR-2002 (first entry)
 DE Human B-cell maturation (BCMA) protein cysteine-rich consensus region.
 XX
 KW Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytosolic; B cell maturation protein; BCMA; tumor necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis.
 XX
 OS Homo sapiens.
 XX
 PN WO200187979-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 14-MAY-2001; 2001WO-US15567.
 XX
 PR 12-MAY-2000; 2000US-204039P.
 PR 27-JUN-2000; 2000US-214591P.
 PR 14-MAY-2001; 2001US-0214591.
 PA (AMGE-) AMGEN INC.
 XX
 PI The111 LE, Yu G;
 XX
 DR WPI; 2002-066686/09.
 XX
 XX Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand -
 XX
 PS Claim 1; Fig 10A; 94pp; English.
 XX
 CC The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA protein cysteine-rich consensus region.
 XX
 SQ Sequence 34 AA;
 Query Match 40.4%; Score 201; DB 23; Length 34;
 Best Local Similarity 100.0%; Pred. No. 7.8e-11;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CSQNEFYDSLHACIPCOLRCSSTNPPLTCQRYC 34
 |||
 Db 1 CSQNEFYDSLHACIPCOLRCSSTNPPLTCQRYC 34

RESULT 5
 AAE15485

ID AAE15485 standard; peptide; 51 AA.

AC AAE15485;

DT 12-MAR-2002 (first entry)

DE Human B-cell maturation (BCMA) protein extracellular domain.

XX Human; transmembrane activator and intracellular CAML interactor; TACI;
 XX cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 XX lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 XX prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 XX drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 XX Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 XX human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 XX rheumatoid arthritis; atherosclerosis.

OS Homo sapiens.

PN WO200187979-A2.

PD 22-NOV-2001.

PF 14-MAY-2001; 2001WO-US15567.

PR 12-MAY-2000; 2000US-204039P.

PR 27-JUN-2000; 2000US-214591P.

PR 14-MAY-2001; 2001US-0214591.

PA (AMGE-) AMGEN INC.

PI The111 LE, Yu G;

DR WPI; 2002-066686/09.

PT Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand -

PS Claim 1; Fig 10A; 94pp; English.

XX The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA protein extracellular domain.

SO Sequence 51 AA;

Query Match 40.4%; Score 201; DB 23; Length 51;

Best Local Similarity 100.0%; Pred. No. 1,1e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CSQNEFYDSLHACIPCOLRCSSTNPPLTCQRYC 34
 |||
 Db 5 CSQNEFYDSLHACIPCOLRCSSTNPPLTCQRYC 38

RESULT 6
 AAE15501

ID AAE15501 standard; peptide; 58 AA.

AC AAE15501;

DT 12-MAR-2002 (first entry)

DE Human B cell maturation protein cysteine rich extracellular region.

XX Human; transmembrane activator and intracellular CAML interactor; TACI;
 XX cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 XX lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 XX prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 XX drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 XX Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 XX human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 XX rheumatoid arthritis; atherosclerosis.

OS Homo sapiens.

PN WO200187979-A2.

PD 22-NOV-2001.

PF 14-MAY-2001; 2001WO-US15567.

PR 12-MAY-2000; 2000US-204039P.

PR 27-JUN-2000; 2000US-214591P.

PR 14-MAY-2001; 2001US-0214591.

PA (AMGE-) AMGEN INC.

PI The111 LE, Yu G;

PT Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand -

PS Disclosure; Fig 13; 94pp; English.

XX The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA cysteine-rich extracellular region.

SO Sequence 58 AA;

Query Match 40.4%; Score 201; DB 23; length 58;
 Best Local Similarity 100.0%; Pred. No. 1.2e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34
 |||||
 Db 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34

RESULT 7
 AAE15484
 ID AAE15484 standard; Protein; 181 AA.
 AC AAE15484;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human B-cell maturation (BCMA) protein.
 XX
 KW Human; transmembrane activator and intracellular CAML interactor; TACI;
 KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 5..38
 FT /note= "Cysteine-rich consensus region: This is region
 FT is specifically claimed as SEQ ID NO: 7 in claim 1 of
 FT the specification"
 FT 52..72
 FT Domain /label= Transmembrane_domain
 FT
 XX
 PN WO200187979-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 14-MAY-2001; 2001WO-US15567.
 XX
 PR 12-MAY-2000; 2000US-204039P.
 BR 27-JUN-2000; 2000US-214591P.
 PR 14-MAY-2001; 2001US-0214591.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI The111 LE, Yu G;
 XX
 DR WPI; 2002-066686/09.
 XX
 PT Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand -
 XX
 PS Disclosure; Fig 10A; 94pp; English.
 XX
 CC The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region, of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function

CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human BCMA protein.
 XX
 SQ Sequence 181 AA;
 XX

Query Match 40.4%; Score 201; DB 23; length 181;
 Best Local Similarity 100.0%; Pred. No. 3.3e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 34
 |||||
 Db 5 CSONEYFDSLHACIPCOLRCSSNTPPLTCORYC 38

RESULT 8
 AAB08843
 ID AAB08843 standard; peptide; 184 AA.
 AC AAB08843;
 XX
 DT 02-JAN-2001 (first entry)
 XX
 DE Amino acid sequence of human.
 XX
 KW BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer;
 KW anti-cell death gene; apoptosis; viral infection; inflammatory response;
 KW rheumatoid arthritis; inflammatory bowel disease; septic shock.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 57..77
 FT /note= "putative transmembrane domain"
 FT
 XX
 PN WO200050633-A1.
 XX
 PD 31-AUG-2000.
 XX
 PF 24-FEB-2000; 2000WO-US04925.
 XX
 PR 24-FEB-1999; 99US-0121485.
 XX
 PA (GENO) GEN HOSPITAL CORP.
 XX
 PI Seed B, Ting A;
 XX
 DR WPI; 2000-558405/51.
 XX
 PT Identifying a modulator of gene expression for drug designing, by
 PT contacting a compound library with a cell expressing an anti-cell death
 PT gene and reporter gene, and determining alteration in reporter gene
 PT expression -
 XX
 PS Claim 32; Fig 7A; 53pp; English.
 XX
 CC The present sequence represents a BCMA (not defined) polypeptide. BCMA
 CC is a necrosis factor (NF)-kB activator. The method of the invention is
 CC used to identify compounds which modulate BCMA activity (and thus NF-kB
 CC activity). The specification describes a method of identifying a
 CC polypeptide which increases gene expression from a promoter. The method
 CC involves contacting a library of with a cell which expresses a
 CC recombinant anti-cell death gene and a reporter gene operably linked to
 CC the promoter, and then determining whether the expression of the
 CC reporter gene is altered as a result of contact with library. The method
 CC is useful for identifying polypeptides which increase or decrease gene
 CC expression from a promoter. The BCMA polypeptide or nucleic acid are
 CC useful for preparing a pharmaceutical composition for treating cancer,

CC apoptosis, viral infections, inflammatory response, such as rheumatoid
 CC arthritis, inflammatory bowel disease or septic shock. BCMA is useful for
 CC identifying compounds that modulate NF-kB expression and thus for drug
 CC designing.

SO Sequence 184 AA;

Query Match 40.4%; Score 201; DB 21; Length 184;
 Best Local Similarity 100.0%; Pred. No. 3,4e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSONEYFDSLHACIPCOLRGSSNTPPLTCORYC 34
 Db 8 GSONEYFDSLHACIPCOLRGSSNTPPLTCORYC 41

RESULT 9
 ID AAY94001 standard; Protein; 184 AA.

AC AAY94001;

DT 20-OCT-2000 (first entry)

XX A human BCMA protein, a B cell protein related to TACI.

XX Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
 KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
 KW znf4 activity; antibody production; autoimmune disease; amyloidosis;
 KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
 KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
 KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;
 KW renal neoplasia; multiple myeloma; lymphoma; light chain neuropathy;
 KW immune response; immunosuppression; graft rejection; joint pain;
 KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
 KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
 KW renal artery stenosis; occlusion; cholesterol; renal emboli.

XX Homo sapiens.

XX WO20040716-A2.

XX 13-JUL-2000.

XX 07-JAN-2000; 2000WO-US00396.

XX 07-JAN-1999; 99US-0226533.

XX (ZYMO) ZYMOGENETICS INC.

XX Gross JA, Xu W, Madden K, Yee DP;

XX MPI; 2000-452538/39.

XX N-PSDB; AAS58559.

XX Inhibiting znf4 activity in a mammal, to treat autoimmune diseases,
 PT renal disease, graft versus host disease, and inflammation, comprises
 PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide -
 XX
 PS Disclosure; Page 152, 175pp; English.

XX The present sequence represents a human BCMA protein, a B cell protein
 CC related to transmembrane activator and CAML-interactor (TACI) receptor.
 CC TACI is a tumour necrosis factor (TNF) receptor. The extracellular
 CC domain of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell
 CC protein) receptor contain a cysteine rich domain, and are used for
 CC inhibiting znf4 activity. Znf4 is a TNF ligand. They may also be used
 CC for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated
 CC with activated or resting B lymphocytes, effector T-cells, or with
 CC antibody production. The antibody production is associated with an
 CC autoimmune disease selected from systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis and rheumatoid arthritis. The znf4 activity
 CC and BR43x2, TACI or BCMA receptor-ligand engagement is associated with

CC asthma, bronchitis, emphysema, end stage renal failure,
 CC glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy,
 CC amyloidosis, moderating immune response, immunosuppression, graft
 CC rejection, graft versus host disease, inflammation, insulin dependent
 CC diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or
 CC septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies,
 CC agonists or antagonists can be used to treat hypertension, renal artery
 CC stenosis, or occlusion, and cholesterol or renal emboli.

SO Sequence 184 AA;

Query Match 40.4%; Score 201; DB 21; Length 184;
 Best Local Similarity 100.0%; Pred. No. 3,4e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSONEYFDSLHACIPCOLRGSSNTPPLTCORYC 34
 Db 8 GSONEYFDSLHACIPCOLRGSSNTPPLTCORYC 41

RESULT 10
 ID AAE09241 standard; Protein; 184 AA.

AC AAE09241;

DT 19-NOV-2001 (first entry)

XX Human BCMA protein.

XX Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
 KW TNFR; TACI; BCMA; therapy; cancer; leukemia; myeloma; lymphoma;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
 KW psoriasis.

XX Homo sapiens.

XX WO200160397-A1.

XX 23-AUG-2001.

XX 28-NOV-2000; 2000WO-US32378.

XX 16-FEB-2000; 2000US-0182938.

XX 22-AUG-2000; 2000US-0226986.

XX (GENTH) GENTENTECH INC.

XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Plicti RM;

XX Yan M;

XX MPI; 2001-541628/60.

XX N-PSDB; AAD15902.
 XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
 PT activity, for treating autoimmune disorders and cancer, comprises
 PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
 PT antagonists -
 XX
 PS Example 2; Fig 2; 160pp; English.

XX The invention relates to methods of using one or more agonists or
 CC antagonists to modulate the activity of the members of TNF (tumour
 CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR)
 CC e.g. TACI or BCMA. The method is useful for treating pathological
 CC conditions or diseases associated with increased TALL-1 and APRIL
 CC expression or activity. TALL-1 and APRIL antagonists are used to
 CC block the interaction between APRIL and TALL-1 with TACI or BCMA.
 CC They are useful for treating a mammal suffering from cancer such
 CC as leukaemia, lymphoma, myeloma, cancers of lung and colon and
 CC autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,
 CC psoriasis and lupus erythematosus. The present sequence is human

CC BCMA protein.
 XX
 SQ Sequence 184 AA;
 Query Match 40.4%; Score 201; DB 22; Length 184;
 Best Local Similarity 100.0%; Pred. No. 3.4e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34
 DB 8 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 41
 RESULT 11
 ID AAE00506 standard; Protein; 184 AA.
 AC AAE00506;
 DT 31-JUN-2001 (first entry)
 DE Human B cell maturation protein (BCMA).
 XX
 KM Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
 KM gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
 KM carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
 KM systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
 KM B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
 KM organ transplantion; HIV; human immunodeficiency virus; TNF;
 KM tumour necrosis factor; BCMA; B cell maturation protein.
 OS Homo sapiens.
 XX
 PN WO200124811-A1.
 XX
 PD 12-APR-2001.
 XX
 PP 05-OCT-2000; 2000WD-US27579.
 XX
 PR 06-OCT-1999; 99US-0157933.
 PR 11-FEB-2000; 2000US-0181807.
 PR 30-JUN-2000; 2000US-0215688.
 XX
 PA (BIOJ) BIOGEN INC.
 XX (APOT-) APOTEC R & D SA.
 PI Schneider P, Thompson J, Cachero T, Ambrose C, Rennett P;
 XX
 DR WPI; 2001-266242/27.
 DR N-PSDB; AAD03844.
 XX
 PT Treating a mammal for a condition associated with undesired cell
 PT proliferation such as cancer or carcinoma, comprises administering a
 PT composition comprising A Proliferation Inducing Ligand Receptor
 PT (APRIL-R) antagonist.
 XX
 PS Claim 3; Fig 3A; 85pp; English.
 XX
 CC The invention relates to a method of treating a mammal for a condition
 CC associated with undesired cell proliferation such as cancer or
 CC carcinoma. The method involves administering a composition comprising
 CC A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as
 CC B cell maturation protein (BCM or BCMA) antagonist that antagonises the
 CC interaction between APRIL and its cognate receptor(s). This method is
 CC useful for treating undesired cell proliferation such as cancer or
 CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
 CC prostate carcinoma, and other carcinomas whose proliferation is modulated
 CC by APRIL. It is also useful for treating autoimmune diseases (Grave's
 CC disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
 CC diseases, renal disorders, B-cell lympho-proliferative disorders,
 CC immunosuppressive diseases, organ transplantion, inflammation and
 CC human immunodeficiency virus (HIV), and for treating, suppressing or
 CC altering an immune response involving a signalling pathway between

CC APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy.
 CC The present sequence is human APRIL-R also referred as BCMA or
 CC BCM protein.
 XX
 SQ Sequence 184 AA;
 Query Match 40.4%; Score 201; DB 22; Length 184;
 Best Local Similarity 100.0%; Pred. No. 3.4e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 34
 DB 8 CSQNEYPDSLHACIPCOLRCSSNTPPLTCQRYC 41
 RESULT 12
 ID AAB60698 standard; Protein; 184 AA.
 AC AAB60698;
 DT 22-MAY-2001 (first entry)
 DE Human BAFF receptor (BAFF-R).
 XX
 KM Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
 KM immune-related disorder; B-cell growth inhibitor; BCMA;
 KM B-cell maturation inhibitor; immunoglobulin production inhibitor;
 KM autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
 KM renal disorder; immunosuppressive disorder; HIV infection;
 KM organ transplantion; antiinflammatory; systemic lupus erythematosus;
 KM autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
 KM B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
 KM lymphoma; gene therapy; cancer; tumour.
 OS Homo sapiens.
 XX
 PN WO200112812-A2.
 XX
 PD 22-FEB-2001.
 XX
 PP 16-AUG-2000; 2000WO-US22507.
 XX
 PR 17-AUG-1999; 99US-0149378.
 PR 11-FEB-2000; 2000US-0181684.
 PR 18-FEB-2000; 2000US-0183536.
 XX
 PA (BIOJ) BIOGEN INC.
 XX (APOT-) APOTEC R & D SA.
 PI Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;
 XX
 DR WPI; 2001-202866/20.
 DR N-PSDB; AAF59998.
 XX
 PT Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
 PT lympho-proliferative disorder by administering BAFF-receptor
 PT polypeptide, chimeric molecule comprising receptor or anti-BAFF-R
 PT antibody homolog.
 XX
 PS Claim 20; Fig 1; 59pp; English.
 XX
 CC The invention relates to the use of a BAFF receptor (BAFF-R, also known
 CC as BCMA) protein, or a BAFF-R fusion protein as an agent for the
 CC treatment of a variety of immune-related disorders. BAFF-R is a member of
 CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
 CC agent, and also plays a role in the development of hypertension and
 CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
 CC specific antibodies can be used for inhibiting B-cell growth, dendritic
 CC cell-induced B-cell growth and maturation, and immunoglobulin production,
 CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative
 CC disorders, hypertension and renal disorders. The BAFF-R proteins may also

CC be used in the treatment of immunosuppressive disorders and HIV
 CC infection, and in patients undergoing organ transplantation. The BAF-R
 CC protein or BAF-R specific antibodies may be used for treating,
 CC suppressing or altering an immune response involving a signalling pathway
 CC between BAF-R and BAF, thereby inhibiting inflammation. Since BAF-R
 CC inhibits B-cell growth and maturation it is useful for treating diseases
 CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
 CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
 CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
 CC human BAF-R may be used in gene therapy to treat tumours, lymphomas,
 CC autoimmune disorders and inherited B-cell-associated disorders. The
 CC present sequence represents human BAF-R.

XX Sequence 184 AA;
 SQ

Query Match 40.4%; Score 201; DB 22; Length 184;
 Best Local Similarity 100.0%; Pred. No. 3.4e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRGSSNTPPLTCORYC 34
 DB 8 CSQNEYFDSLHACIPCOLRGSSNTPPLTCORYC 41

RESULT 13
 AAY71979 standard; Protein; 184 AA.

XX AAY71979;
 AC
 XX
 DT 28-MAR-2001 (first entry)

XX Human B cell maturation factor (BCMA) protein.

XX
 DE
 XX
 KW Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
 KW Tumour necrosis factor and Apol-related leucocyte expressed ligand 1;
 KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
 KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
 KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
 KW haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16;
 KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
 KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.

XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT Domain 1..62
 FT /label= Extracellular_domain

XX
 FN WO200068378-A1.

XX
 PD 16-NOV-2000.

XX
 PE 05-MAY-2000; 2000WO-US12266.

XX
 PR 06-MAY-1999; 99US-0132892.
 PR 01-MAY-2000; 2000US-0201012.

XX
 PA (NAJE-) NAT JEWISH MEDICAL & RES CENT.

XX
 PI Shu HS;

XX
 XX WPI; 2001-016094/02.
 DR N-Psdb; AAD02125.

XX
 XX Isolated TALL-1 protein is used to identify compounds that regulate B
 PT lymphocyte proliferation, used to treat B lymphocyte associated
 PT autoimmune disorders -

XX
 PS Claim 37; Page 104-105; 112pp; English.

XX
 CC The present invention relates to Tumour necrosis factor (TNF) and
 CC Apol-related leucocyte expressed ligand 1 (TALL-1) nucleic acid

CC molecules, proteins (including homologues), and their antibodies. The
 CC invention in particular relates to methods for regulating the
 CC interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell
 CC maturation factor) to regulate monocyte, macrophage and B lymphocyte
 CC mediated immune responses. TALL-1 protein is useful for identifying
 CC compounds that regulate B lymphocyte proliferation. It is also useful for
 CC treating B lymphocyte associated autoimmune disorders like rheumatoid
 CC arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes
 CC mellitus, multiple sclerosis, myasthenia gravis, Grave's disease,
 CC autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura,
 CC Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever,
 CC post-streptococcal glomerulonephritis, or polyarteritis nodosa.
 CC The TALL-1 protein and its corresponding nucleic acid sequence are also
 CC useful in diagnostic assays.

CC The present sequence is a human B cell maturation factor (BCMA)
 CC protein. It is the receptor for TALL-1 protein. BCMA gene is
 CC located on chromosome 16. In human tissues, BCMA is expressed by
 CC spleen and lymph nodes but not by brain, muscle, heart, lung, kidney,
 CC pancreas, testis and placenta. BCMA mRNA is absent in the pro-B
 CC lymphocyte stage but its expression increases with B lymphocyte
 CC maturation.

XX Sequence 184 AA;
 SQ

Query Match 40.4%; Score 201; DB 22; Length 184;
 Best Local Similarity 100.0%; Pred. No. 3.4e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRGSSNTPPLTCORYC 34
 DB 8 CSQNEYFDSLHACIPCOLRGSSNTPPLTCORYC 41

RESULT 14
 ABB81487 standard; Protein; 184 AA.

XX ABB81487;
 AC
 XX
 DT 02-SEP-2002 (first entry)

XX Human BCMA receptor related protein SEQ ID NO:7.

XX
 DE
 XX
 KW Human; Znfir12; tumour necrosis factor receptor; cytosstatic;
 KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;
 KW neuroprotective; antirheumatic; antiarthritic; antiaesthatic;
 KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
 KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
 KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
 KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
 KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
 KW pyelonephritis; renal neoplasia; multiple myeloma; amyloidosis;
 KW light chain neuropathy; hypertension; large vessel disease;
 KW graft-versus host disease; graft rejection; Crohn's disease.

XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT Domain 1..62
 FT /label= Extracellular_domain

XX
 FN WO200238766-A2.

XX
 PD 16-MAY-2002.

XX
 PE 05-NOV-2001; 2001WO-US47018.

XX
 PR 07-NOV-2000; 2000US-24649P.
 PR 20-DEC-2000; 2000US-257131P.
 PR 28-JUN-2001; 2001US-301715P.
 PR 29-AUG-2001; 2001US-315565P.

XX
 PA (ZYMO) ZYMOGENETICS INC.

XX
 PI Gross JA, Xu W, Heme RM, Grant FJ;

XX
 XX WPI; 2002-508212/54.

XX Novel isolated human tumor necrosis factor receptor polypeptide, termed
 PT Znfir12, useful for treating autoimmune disorders, emphysema, end
 stage renal failure or renal disease and lymphoma -
 XX
 PS Disclosure; Page 135-136; 154pp; English.

XX The present invention describes a human tumour necrosis factor receptor
 CC designated Znfir12 (I). (I) has cytostatic, immunosuppressive,
 CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
 CC antineumatic, antirheumatic, antiaspheric, nephrotoxic and hypotensive
 CC activities, and can be used in gene therapy. (I) can be used for
 CC inhibiting, in a mammal, the activity of a ligand that binds Znfir12
 CC (e.g. ZTNF4), for treating disorders and diseases associated with B
 CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
 CC inhibiting the proliferation of tumour cells. (I) is useful for treating
 CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
 CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
 CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
 CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
 CC leukaemia, nephritis, and pyelonephritis, and for treating renal
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
 CC amyloidosis, hypertension, large vessel diseases, graft-versus host
 CC disease, graft rejection and Crohn's disease. (I) is useful for
 CC modulating the immune system, for regulating B cell responses and
 CC development, for modulating development of other cells, antibody
 CC production and cytokine production, and for modulating T and B cell
 CC communication. The present sequence represents a protein which is
 CC given in the exemplification of the present invention.

XX Sequence 184 AA;
 SQ

Query Match 40.4%; Score 201; DB 23; Length 184;
 Best Local Similarity 100.0%; Pred. No. 3,4e-10;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CSQNEFYDSLHACIPQCRSSNTPTLCQRYC 34
 Db 8 CSQNEFYDSLHACIPQCRSSNTPTLCQRYC 41

RESULT 15
 AAB60700
 ID AAB60700 standard; Protein; 157 AA.
 XX
 AC AAB60700;
 XX
 DT 22-MAY-2001 (first entry)
 XX
 XX Human BAPF receptor (BAPF-R) sequence encoded by A plasmid pJST535.
 KW Human BAPF-R; BAPF receptor; TNF family; immunoregulatory agent;
 KW immune-related disorder; B-cell growth inhibitor; BCMA; inhibitor;
 KW B-cell maturation inhibitor; immunoglobulin production inhibitor;
 KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
 KW renal disorder; immunosuppressive disorder; HIV infection;
 KW organ transplantation; antiinflammatory; systemic lupus erythematosus;
 KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
 KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
 KW lymphoma; gene therapy; cancer; tumour; plasmid pJST535.
 KW
 XX Homo sapiens.
 OS
 XX WO200112812-A2.
 PN
 PD 22-FEB-2001.
 XX
 PF 16-AUG-2000; 2000WD-US22507.
 XX
 PR 17-AUG-1999; 99US-0149378.
 PR 11-FEB-2000; 2000US-0181684.
 PR 18-FEB-2000; 2000US-0183536.
 XX

PA (BIOJ) BIOGEN INC.
 PA (APOT-) APOTTECH R & D SA.
 XX
 XX Mackay F, Browning J, Ambrose C, Teschopp J, Schneider P;
 PI Thompson J;
 XX
 XX WPI; 2001-202866/20.
 DR N-PSDB; AAF60000.
 XX
 XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
 PT lymphoproliferative disorder by administering BAPF-receptor
 PT polypeptide, chimeric molecule comprising receptor or anti-BAPF-R
 PT antibody homolog -
 XX
 XX Example 1; Fig 3; 59pp; English.

XX The invention relates to the use of a BAPF receptor (BAPF-R, also known
 CC as BCMA) protein, or a BAPF-R fusion protein as an agent for the
 CC treatment of a variety of immune-related disorders. BAPF-R is a member of
 CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory
 CC agent, and also plays a role in the development of hypertension and
 CC related disorders. BAPF-R, fusion proteins containing it, and BAPF-R-
 CC specific antibodies can be used for inhibiting B-cell growth, dendritic
 CC cell-induced B-cell growth and maturation, and immunoglobulin production,
 CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative
 CC disorders, hypertension and renal disorders. The BAPF-R proteins may also
 CC be used in the treatment of immunosuppressive disorders and HIV
 CC infection, and in patients undergoing organ transplantation. The BAPF-R
 CC proteins or BAPF-R specific antibodies may be used for treating,
 CC suppressing or altering an immune response involving a signalling pathway
 CC between BAPF-R and BAPF, thereby inhibiting inflammation. Since BAPF-R
 CC inhibits B-cell growth and maturation it is useful for treating diseases
 CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
 CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
 CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
 CC human BAPF-R may be used in gene therapy to treat tumours, lymphomas,
 CC autoimmune disorders and inherited B-cell-associated disorders. The
 CC present sequence represents a human BAPF-R protein sequence as encoded
 CC by plasmid pJST535. However, this BAPF-R protein sequence is 27 amino
 CC acids shorter than that given in AAB60698.

XX Sequence 157 AA;
 SQ

Query Match 32.0%; Score 159.5; DB 22; Length 157;
 Best Local Similarity 90.6%; Pred. No. 1,1e-06;
 Matches 29; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

OY 3 ONEYFDSLHACIPQCRSSNTPTLCQRYC 34
 Db 7 ONEYFDSLHACIPQCRSSNTPTLCQRYC 35

Search completed: February 4, 2003, 12:57:44
 Job time : 21.6599 secs

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OM protein - protein search, using SW model

Run on: February 4, 2003, 12:53:41 / Search time 17.3806 Seconds
(without alignments)
960.257 Million cell updates/sec

Title: US-09-854-864-13

Perfect score: 498

Sequence: 1 CSQNEFDSLHACIPQCLR.....SEYFDSLHACPPATCPYC 81

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_phc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_prodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.5	20.2	1792	13	057484 gallus gall
2	94.5	19.0	223	11	062220 mus musculu
3	94.5	19.0	230	11	064507 mus musculu
4	93.5	18.8	195	11	09D141 mus musculu
5	92.5	18.6	169	4	014564 mus musculu
6	92.5	18.6	227	11	09D225 mus musculu
7	91.5	18.4	136	4	09BYR2 mus sapien
8	91.5	18.4	186	4	09BYR2 mus sapien
9	91.5	18.4	186	11	064526 mus musculu
10	91.5	18.4	191	11	09D3H7 mus musculu
11	89	17.9	159	4	09BYQ3 mus sapien
12	89	17.9	1574	11	088281 rattus norv
13	88	17.7	166	4	09BYR3 mus sapien
14	87.5	17.6	154	4	09BYQ2 mus sapien
15	87.5	17.6	174	4	09BYQ4 mus sapien
16	87.5	17.6	193	4	09BYQ5 mus sapien

17	87	17.5	159	4	09BYQ0 mus sapien
18	87	17.5	165	11	09D7P3 mus musculu
19	87	17.5	195	11	09D0X9 mus musculu
20	87	17.5	1376	5	08SZS2 drosophila
21	87	17.5	1679	5	024301 drosophila
22	86	17.3	188	11	070148 rattus norv
23	86	17.3	2112	5	08WPU0 mus sapien
24	85.5	17.2	154	4	09BYP9 mus sapien
25	85.5	17.2	177	11	09D644 mus musculu
26	85.5	17.2	189	11	09D527 mus musculu
27	85	17.1	202	11	091W93 mus musculu
28	85	17.1	325	10	094HS1 mus sapien
29	84.5	17.0	767	13	09DGR2 mus sapien
30	84	16.9	195	4	09BYQ6 mus sapien
31	84	16.9	201	4	09BQ06 mus sapien
32	84	16.9	210	4	09BYR0 mus sapien
33	84	16.9	1671	5	09NJV5 mus sapien
34	83.5	16.8	110	5	09BIR2 mus sapien
35	83.5	16.8	130	11	09Z287 mus sapien
36	83.5	16.8	191	4	09BYQ8 mus sapien
37	83	16.7	175	4	007628 mus sapien
38	82	16.5	98	4	09BYR8 mus sapien
39	82	16.5	126	6	028707 oryctolagus
40	82	16.5	167	11	09D122 mus musculu
41	82	16.5	168	11	09D732 mus musculu
42	81.5	16.4	85	11	070555 mus musculu
43	81.5	16.4	429	13	091650 xenopus lae
44	81	16.3	353	5	09VW81 drosophila
45	81	16.3	353	5	08SZS8 drosophila

ALIGNMENTS

RESULT 1

ID 057484 PREDIMINARY; PRT; 1792 AA.

AC 057484;
01-JUN-1998 (TREMUREL.06, Created)

DT 01-JUN-1998 (TREMUREL.06, Last sequence update)

DT 01-JUN-2002 (TREMUREL.21, Last annotation update)

DE Lamnin beta 2-like chain.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.

CC NCBI_TaxID=9031;

CX [1]

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93015947; PubMed=1400373;
"A novel lamnin B1 chain variant in avian eye.";

RA O'Rear J.J.;
J. Biol. Chem. 267:20555-20557 (1992).

RL [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=98209634; PubMed=9550264;
Liu J., Swadlow S., Xie W., Brewton R.G., Mayne R.;
evidence for four beta chains in birds.";

RT "Primary structure and expression of a chicken lamnin beta chain:
Matrix Biol. 16:471-481 (1998).

RL EMBL; AF038555; AAB92586.1; -.

DR HSSP; P02468; IKLO.

DR InterPro; IPR002106; AATRNA_ligaseII.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR002049; Lamnin_EGF.

DR InterPro; IPR001866; Lamnt.

DR Pfam; PF00053; lamnin_EGF; 13.

DR Pfam; PF00053; lamnin_Nterm; 1.

DR PRINTS; PR00011; EGFATININ.

DR SMART; SMO0180; EGF_Iam; 13.

DR SMART; SMO0136; Lamnt; 1.

DR PROSITE; PS00339; AA_TENA_LIGASE_II_2; UNKNOWN_1.

DR PROSITE; PS00022; EGF_1; UNKNOWN_10.

DR PROSITE: PS01186; EGF 2; 2.
 DR PROSITE: PS01248; LAMININ_TYPE_EGF_12.
 KM EGF-like domain; GLYCOPROTEIN; Laminin EGF-like domain; Repeat.
 SQ SEQUENCE 1792 AA; 195723 MW; 4A4CBE0206FA600 CRC64;

Query Match 20.2%; Score 100.5; DB 13; Length 1792;
 Best Local Similarity 32.0%; Pred. No. 0.00059;
 Matches 32; Conservative 8; Mismatches 35; Indels 25; Gaps 6;

QY 1 CSQNEFYDSLHACIPQCRSSNTPPLTCQRYCCFYDSLHACPCRCSPPTQYCCF 49
 DB 1017 CQPGYGDAMRHS---RRCSCNTLTGTDPNTCGPQCCDQSGGCHCLPHVEGSCSR 1072
 QY 50 CSP-----PTQYCCFHSFYDSLHACPCRCSPATQPYC 81
 DB 1073 CSPNFMNLGSGGCEPCACGPH--SLSPACNQPTGQSCC 1110

RESULT 2

Q62220 PRELIMINARY; PRT; 223 AA.
 AC Q62220;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DE Serine 2 ultra high sulfur protein.
 GN KRTAP5-4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RC STRAIN=BALB/C;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91065960; PubMed=2250030;
 RA Wood L., Mills M., Hatzembuhler N., Vogel G.;
 RT "Serine-rich ultra high sulfur protein gene expression in murine hair
 and skin during the hair cycle.";
 RL J. Biol. Chem. 265:21375-21380(1990).
 RN [2]
 RC SEQUENCE FROM N.A.
 RX STRAIN=BALB/C;
 MEDLINE=91154184; PubMed=1840598;
 RA Wood L., Mills M., Hatzembuhler N., Vogel G.;
 RT "Additions and Corrections: Serine-rich ultra high sulfur protein gene
 expression in murine hair and skin during the hair cycle.";
 RL J. Biol. Chem. 266:4024-4024(1991).
 DR HSEB; M37760; AAA40107.1; -.
 DR HSEB; P01064; IPT2.
 DR MGD; MGI:1354758; Krtap5-4.
 DR InterPro; IPR001450; 4Fe4S_ferredoxin.
 DR InterPro; IPR001007; VWF_C.
 DR PROSITE; PS00198; 4FE4S_FERRDOXIN; UNKNOWN_2.
 DR PROSITE; PS01208; VWF_C; UNKNOWN_2; C654BDB9FD08C59A CRC64;
 SQ SEQUENCE 223 AA; 21442 MW; C654BDB9FD08C59A CRC64;

Query Match 19.0%; Score 94.5; DB 11; Length 223;
 Best Local Similarity 29.6%; Pred. No. 0.00052;
 Matches 24; Conservative 3; Mismatches 27; Indels 27; Gaps 5;

QY 1 CSQNEFYDSLHACIPQCRSSNTPPLTCQRYCCFYDSLHACPCRCSPPTQYCCF 60
 DB 150 CCSS-----CCKPC-----CSCGSSCCGSSCC-----PCC-CGSSCCPKCC 189
 QY 61 HSEFYDSLHACPCRCSPATQPYC 81
 DB 190 QSS-----CCKPCCGSSC 203

RESULT 3
 Q64507 PRELIMINARY; PRT; 230 AA.
 AC Q64507;

DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Serine 1 ultra high sulfur protein.
 GN KRTAP5-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RC STRAIN=BALB/C;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91065960; PubMed=2250030;
 RA Wood L., Mills M., Hatzembuhler N., Vogel G.;
 RT "Serine-rich ultra high sulfur protein gene expression in murine hair
 and skin during the hair cycle.";
 RL J. Biol. Chem. 265:21375-21380(1990).
 DR HSEB; M37759; AAA40106.1; -.
 DR HSEB; P01064; IPT2.
 DR MGD; MGI:1354732; Krtap5-1.
 DR InterPro; IPR001450; 4Fe4S_ferredoxin.
 DR InterPro; IPR000020; Anaphylatoxin.
 DR InterPro; IPR001305; DnaJ_CXXCXXG.
 DR InterPro; IPR001007; VWF_C.
 DR PROSITE; PS00198; 4FE4S_FERRDOXIN; UNKNOWN_1.
 DR PROSITE; PS01177; ANAPHYLATOXIN_1; UNKNOWN_1.
 DR PROSITE; PS00637; DnaJ_CXXCXXG; UNKNOWN_1.
 DR PROSITE; PS01208; VWF_C; UNKNOWN_3.
 SQ SEQUENCE 230 AA; 21781 MW; FCC50B41B2137C23 CRC64;

Query Match 19.0%; Score 94.5; DB 11; Length 230;
 Best Local Similarity 29.6%; Pred. No. 0.00053;
 Matches 24; Conservative 3; Mismatches 27; Indels 27; Gaps 5;

QY 1 CSQNEFYDSLHACIPQCRSSNTPPLTCQRYCCFYDSLHACPCRCSPPTQYCCF 60
 DB 149 CCSS-----CCKPC-----CSCGSSCCGSSCC-----PCC-CGSSCCPKCC 188
 QY 61 HSEFYDSLHACPCRCSPATQPYC 81
 DB 189 QSS-----CCKPCCGSSC 202

RESULT 4

Q6D141 PRELIMINARY; PRT; 195 AA.
 AC Q6D141;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE 18 days embryo cDNA, RIKEN full-length enriched library,
 DE clone:1110030N11, full insert sequence.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6J; TISSUE=EMBRYO;
 MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aikawa T., Hara A., Fukunishi Y., Kono H., Adachi U., Fukuda S.,
 RA Aikawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kato K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barab G.,
 RA Blake J., Boffelli D., Bojunga N., Carlini P., de Bonaudo M.F.,
 RA Brownstein M.J., Bult C., Flechner C., Fujita M., Gariboldi M.,
 RA Guenichon S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzairelli J., Mombaerts P.,

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SCALP;
 RA Rogers M.A., Langbein L., Winter H., Ehmann C., Korn B., Schweizer J.;
 RT "Characterization of a cluster of human high/ultrahigh keratin
 associated proteins on chromosome 17q12-21";
 RL Submitted (OCT-2000) to the EMBL/Genbank/DBD databases.
 DR EMBL; AJ406934; CAC27573.1; -
 DR InterPro; IPR002494; Keratin B2.
 DR InterPro; IPR001368; TNFR_C6.
 DR Pfam; PF01500; Keratin B2; 1.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
 SQ SEQUENCE 136 AA; 14402 MW; 51E51463925E02E CRC64;

Query Match 18.4%; Score 91.5; DB 4; Length 136;
 Best Local Similarity 29.7%; Pred. No. 0.00079;
 Matches 27; Conservative 5; Mismatches 38; Indels 21; Gaps 5;

QY 10 LHAACP--COLRC-----SSNTPPLTCQRYCCYFDSLHAC--PCLR---C 50
 DB 17 LENCPCPSCCQTTCCRTCCRPSCCVSSCCRPCCQSVCCQPTCCSCCQTTCCRTCC 76
 QY 51 SPPTCYCCFHFSEYFDSLHACPPATCPYC 81
 DB 77 RSCCVSSCFRPCCQSV--CCQPTCCRPSC 105

RESULT 8

Q9BYR2 PRELIMINARY; PRT; 186 AA.

DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-APR-2002 (TRENBLrel. 20, Last annotation update)
 DE Keratin associated protein 4.5.

GN KRTPA.5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SCALP;
 RA Rogers M.A., Langbein L., Winter H., Ehmann C., Korn B., Schweizer J.;
 RT "Characterization of a cluster of human high/ultrahigh keratin
 associated proteins on chromosome 17q12-21";
 RL Submitted (OCT-2000) to the EMBL/Genbank/DBD databases.
 DR EMBL; AJ406937; CAC27576.1; -
 DR InterPro; IPR002494; Keratin B2.
 DR InterPro; IPR001304; Lectin C.
 DR InterPro; IPR001368; TNFR_C6.
 DR InterPro; IPR001007; VWF_C.
 DR Pfam; PF01500; Keratin B2; 1.
 DR PROSITE; PS00652; C_TYFE_LECTIN_1; UNKNOWN_1.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE; PS01208; VWF_C; UNKNOWN_2.
 SQ SEQUENCE 186 AA; 19916 MW; 034D9C7343D4F63A CRC64;

Query Match 18.4%; Score 91.5; DB 4; Length 186;
 Best Local Similarity 30.5%; Pred. No. 0.001;
 Matches 25; Conservative 6; Mismatches 28; Indels 23; Gaps 6;

QY 10 LHAACP--COLRCSSNT--PPLTCQRYCCYFDSLHACPCRLCSPPTC-----QYCC 59
 DB 17 LENCPCPSCCQTTCCRTCCRPSCCVSSCCRPCCQSVCCQPTCCSCCQTTCCRTCC 71
 QY 60 FHFSEYFDSLHACPPATCPYC 81
 DB 72 FESS-----CCRPCCRPSC 85

RESULT 9

064526

ID 064526 PRELIMINARY; PRT; 186 AA.

AC Q64526;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-APR-2002 (TRENBLrel. 20, Last annotation update)
 DE Ultra-high sulphur keratin.
 GN KRTP9-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=89140394; PubMed=2465353;
 RA McNab A.R., Wood L., Threlkelt N., Gierman T., Vogel G.;
 RT "An ultra-high sulfur keratin gene is expressed specifically during
 hair growth";
 RL J. Invest. Dermatol. 92:263-266(1989).
 CC -1. SIMILARITY: TO THE PLANT THIONIN FAMILY.
 DR EMBL; M27685; AA81560.1; -
 DR MGD; MGI:130997; Krtap9-1.
 DR InterPro; IPR002494; Keratin B2.
 DR InterPro; IPR001010; Thionin.
 DR InterPro; IPR001368; TNFR_C6.
 DR InterPro; IPR001007; VWF_C.
 DR Pfam; PF01500; Keratin B2; 1.
 DR PROSITE; PS00271; THIONIN; 1.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE; PS01208; VWF_C; UNKNOWN_1.
 SQ SEQUENCE 186 AA; 19658 MW; 61D6BDBA72CFEB4 CRC64;

Query Match 18.4%; Score 91.5; DB 11; Length 186;
 Best Local Similarity 34.7%; Pred. No. 0.001;
 Matches 25; Conservative 4; Mismatches 24; Indels 19; Gaps 6;

QY 14 CLP--COLRC--SSNTPPLTCQRYCCYFDSLHAC--PCLRCSPPTCYCCFHFSEYFDSL 69
 DB 85 CQPCQPCSCCQSSCCQPCRCSSCCQPCRCISSCCQPC--CRPSCCQSSC----- 132
 QY 70 HACPPATCPYC 81
 DB 133 --CRPC--CQPC 141

RESULT 10

Q9D3H7 PRELIMINARY; PRT; 191 AA.

DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE 10 days neonate head cDNA, RIKEN full-length enriched library,
 clone:5530401L02, full insert sequence.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=HEAD;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Iehi Y.,
 RA Aikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiraldi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barab G.,
 RA Blake J., Boffelli D., Bojunga N., Carmignani P., de Bonaldo M.F.,
 RA Brownstein M.J., But C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guetlich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Marzarelli J., Momberte P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shihata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitteker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlschki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL: AK017437; BAB30743.1; -.
DR InterPro: IPR002494; Keratin_B2.
DR InterPro: IPR001010; Thionin.
DR InterPro: IPR001368; TNFR_c6.
DR InterPro: IPR001007; VWF_C.
DR Pfam: PF01500; Keratin_B2; 1.
DR PROSITE: PS00271; THIONIN; UNKNOWN_1.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS01208; VWFc UNKNOWN_1.
SQ SEQUENCE 191 AA; 2008 MW; 522B841DC9A8A9D5 CRC64;

Query Match 18.4%; Score 91.5; DB 11; Length 191;
Best Local Similarity 32.9%; Pred. No. 0.0011;
Matches 23; Conservative 3; Mismatches 21; Indels 23; Gaps 5;

OY 16 PCQLRCSNTP---PLTCRYCCYFDSILHACPCRCSPPTCO-YCCFHSYFDSILHA 71
DB 63 PCCVSSCCRTPCPCPCCCVSSCCQ-----PC--CQPSCCQSSCCQPS-----C 103

OY 72 CPATCOPYC 81
DB 104 CQPSCCQPS 113

RESULT 11
O9BY03 PRELIMINARY; PRT; 159 AA.

ID O9BY03
AC O9BY03
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE Keratin associated protein 9.3.

CN KRTP9.3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=SCALP;
RA Rogers M.A., Langbein L., Winter H., Ehmann C., Korn B., Schweizer J.,
RT "Characterization of a cluster of human high/ ultrahigh keratin
RT associated proteins on chromosome 17q12-21."
RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL: AJ406947; CAC27586.1; -.
DR InterPro: IPR002494; Keratin_B2.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF01500; Keratin_B2; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.

SQ SEQUENCE 159 AA; 1653 MW; 375CC1E52ECCB68 CRC64;

Query Match 17.9%; Score 89; DB 4; Length 159;
Best Local Similarity 29.5%; Pred. No. 0.0018;
Matches 26; Conservative 4; Mismatches 20; Indels 38; Gaps 7;

OY 10 LHAACIP-CQLARC-----SSNTPLTCORYCCYFDSILHAC--PCLRCSP 53
DB 1 MHCCSPCCQPCPCRTTCQPTVTTCSSTP--CCQPSCC-----VSSCCQPC--CHPT 50

OY 54 TCQYCCFHSYFDSILHACPCATCOPYC 81
DB 51 CCQNTC-----CRITCCQPCIC 66

RESULT 12

O88281
ID O88281 PRELIMINARY; PRT; 1574 AA.

AC O88281
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MEGP6.

GN MEGP6.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE=98360089; Pubmed=9693030;
RA Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.,
RT "Identification of high-molecular-weight proteins with multiple EGF-
RT like motifs by motif-trap screening."
RL Genomics 51:27-34(1998).

DR EMBL: AB011532; BAA32462.1; -.
DR HSSP: P00736; IAPQ.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.

DR Pfam: PF00008; EGF; 24.
DR SMART: SM00179; EGF_CA; 4.
DR SMART: SM00001; EGF_like; 19.

DR PROSITE: PS00010; ASX_HYDROXYL; 5.
DR PROSITE: PS00022; EGF_1; UNKNOWN_23.
DR PROSITE: PS01186; EGF_2; 23.
DR PROSITE: PS01187; EGF_CA; 5.

DR KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
SQ SEQUENCE 1574 AA; 16544 MW; 2B4853D8F7F6E7 CRC64;

Query Match 17.9%; Score 89; DB 11; Length 1574;
Best Local Similarity 29.4%; Pred. No. 0.014;
Matches 30; Conservative 9; Mismatches 25; Indels 38; Gaps 8;

OY 1 CSQNYFDSILHACIPQCL-----RCSNTPLT-----CQRYCCY-----PDSILHACPC 47
DB 966 CSAGAPCDVATGSCI-CPAGRWGRPCQSCPLTYGLNCSQCTCFNGASCDSTVTCQ-- 1022

OY 48 LRCSF-----PTCYCCFHSYFDSILHACPPA---TCQPYC 81
DB 1023 -HCARGMGPTC-----LQACPELYGKNCQHC 1050

RESULT 13
O9BYR3 PRELIMINARY; PRT; 166 AA.

ID O9BYR3
AC O9BYR3
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Keratin associated protein 4.4.

CN KRTP4.4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=SCALP;
RA Rogers M.A., Langbein L., Winter H., Ehmann C., Korn B., Schweizer J.,
RT "Characterization of a cluster of human high/ ultrahigh keratin
RT associated proteins on chromosome 17q12-21."
RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL: AJ406936; CAC27575.1; -.
DR InterPro: IPR002494; Keratin_B2.
DR InterPro: IPR001368; TNFR_c6.
DR InterPro: IPR001007; VWF_C.
DR Pfam: PF01500; Keratin_B2; 1.

DR PROSITE; PS00652; TNFR_NGFR.1; UNKNOWN_1.
DR PROSITE; PS01208; VWF; UNKNOWN_1.
SQ SEQUENCE 166 AA; 18023 MW; C37D121611A7115 CRC64;

Query Match 17.7%; Score 88; DB 4; Length 166;
Best Local Similarity 28.4%; Pred. No. 0.0025; Indels 30; Gaps 5;
Matches 25; Conservative 4; Mismatches 29;

QY 10 LHAACP-CQLRC-----SSNTPPLTCQRYCEYFDSLHAACPCLR--CSP 53
DB 17 LENCGRPSYQTTTCRTTCRPSGCVSSCCRPCCQTTCCR--TTCCHPSCVSSCCRPQ 74

QY 54 TCQYCCFHSYFDSLHAACPATCQPYC 81
DB 75 CCQSV-----CQPTCCRPQC 90

RESULT 14

Q9BYQ2 PRELIMINARY; PRT; 154 AA.

AC Q9BYQ2; 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE Keratin associated protein 9.4.

GN KRTAP9.4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
RP SEQUENCE FROM N.A.

RA Rogers M.A., Langbein L., Winter H., Ehmann C., Korn B., Schweizer J.,
RT "Characterization of a cluster of human high/ultrahigh keratin
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ406948; CAC27587.1; -
DR InterPro; IPR002494; Keratin B2.
DR Pfam; PF01500; Keratin B2; 1

SQ SEQUENCE 154 AA; 16454 MW; 2EAF62E16165105 CRC64;

Query Match 17.6%; Score 87.5; DB 4; Length 154;
Best Local Similarity 26.4%; Pred. No. 0.0027;
Matches 29; Conservative 10; Mismatches 30; Indels 41; Gaps 8;

QY 1 CSQNEFYFD--SLHAACP-----CQLRC-----SSNTPPLTCQRYCEYFDS----- 40
DB 56 CCQNTCCQPTCVTSCCPSCSTPCQPTCCGSSCDQSSCAVYCRKTC--YPTTVCL 113

QY 41 ---LHAAC-----PCLRCSPPTCQYCCFHSYFDSLHAACPATCQPYC 81
DB 114 PGLNCSGCSNCCQPC--CRPACETTCFP-----TCVYSCCQPC 153

RESULT 15

Q9BYQ4 PRELIMINARY; PRT; 174 AA.

AC Q9BYQ4; 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE Keratin associated protein 9.2.

GN KRTAP9.2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RA Rogers M.A., Langbein L., Winter H., Ehmann C., Korn B., Schweizer J.,
RT "Characterization of a cluster of human high/ultrahigh keratin

RT associated proteins on chromosome 17q12-21."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ406946; CAC27585.1; -
DR InterPro; IPR002494; Keratin B2.
DR Pfam; PF01500; Keratin B2; 1
SQ SEQUENCE 174 AA; 18261 MW; 2C378CFB0AA9F24D CRC64;

Query Match 17.6%; Score 87.5; DB 4; Length 174;
Best Local Similarity 28.6%; Pred. No. 0.003;
Matches 26; Conservative 4; Mismatches 22; Indels 39; Gaps 7;

QY 10 LHAACP-CQLACSSNT-----PPLT-----CQRYCEYFDSLHAAC--PCLRC 50
DB 1 WTHCSPPCCQPTTCRTTCRTTCWKRPVTYTCSTSTSCQPACC-----VSSCCQPC--C 52

QY 51 SPPTCQYCCFHSYFDSLHAACPATCQPYC 81
DB 53 RPTSCQNTC-----CRTCCQPTC 71

Search completed: February 4, 2003, 12:59:08
Job time : 18.3806 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 4, 2003, 12:53:16 ; Search time 5.5749 Seconds
(without alignments)
602.627 Million cell updates/sec

Title: US-09-854-864-13

Perfect score: 498
Sequence: 1 CSQNEPFDILHACIPQLR.....SEYFDSLHACPPATCPYC 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	201	40.4	184	TR17_HUMAN	Q02223 homo sapien
2	136	27.3	185	TR17_MOUSE	O08472 mus musculu
3	98	19.7	249	T13X_MOUSE	Q96c35 mus musculu
4	93	18.7	293	T13X_HUMAN	O14836 homo sapien
5	92.5	18.6	169	KRUA_HUMAN	P26371 homo sapien
6	91	18.3	194	KRUB_HUMAN	O76990 homo sapien
7	87	17.5	1680	PUR2_DROME	P30432 drosophila
8	86.5	17.4	1877	PCRS_MOUSE	Q04592 mus musculu
9	83	16.7	131	KRA3_SHEEP	P02441 oviss aries
10	82	16.5	526	UBPW_MOUSE	Q61068 mus musculu
11	81	16.3	1587	LMG3_HUMAN	O63415 rattus norv
12	80.5	16.2	937	PAC4_RAT	P55268 homo sapien
13	80.5	16.2	1798	LMB2_HUMAN	P25391 homo sapien
14	80	16.1	3075	LMW1_HUMAN	P58391 saccharomyc
15	79.5	16.0	965	YNC3_YEAST	P98092 bombayx mori
16	79.5	16.0	3133	HMCT_BOMMO	O9n15 branchiosteo
17	79	15.9	1696	PKCS_BACAL	P03442 capra hircu
18	77.5	15.6	132	KRA3_CAPII	O43609 homo sapien
19	77.5	15.6	139	SPY1_HUMAN	P02441 oviss aries
20	77	15.5	171	KR2A_SHEEP	O08799 mus musculu
21	77	15.5	5376	ZAN_MOUSE	O09472 homo sapien
22	76.5	15.4	2414	P300_HUMAN	P45481 mus musculu
23	76	15.3	2441	CBP_MOUSE	O16787 homo sapien
24	75.5	15.2	1713	LMW3_HUMAN	O970b6 mus musculu
25	75	15.1	1581	LMG3_MOUSE	P11047 homo sapien
26	75	15.1	1609	LMG1_HUMAN	Q28065 bos taurus
27	74.5	15.0	610	CABP_BOVIN	P07942 homo sapien
28	74	14.9	1786	LMW1_MOUSE	O92793 mus musculu
29	74	14.9	2442	CBP_HUMAN	O61292 mus musculu
30	73.5	14.8	313	SPY1_MOUSE	P26122 homo sapien
31	73.5	14.8	1799	LMW2_MOUSE	Q09930 g sortilin-
32	72.5	14.6	969	PAC4_HUMAN	
33	72.5	14.6	1592	SORTL_CHICK	

34	72	14.5	575	1	TRBM_HUMAN	P07204 homo sapien
35	72	14.5	867	1	SSPO_BOVIN	P98167 bos taurus
36	72	14.5	1367	1	IGIR_HUMAN	P08069 homo sapien
37	72	14.5	1700	1	BAR3_CHITE	Q03376 chironomus
38	72	14.5	2569	1	LMW3_MOUSE	O61789 mus musculu
39	72	14.5	4655	1	LRP2_HUMAN	P98164 homo sapien
40	71.5	14.4	1435	1	EBAL_PLAFC	P19214 plasmodium
41	71	14.3	62	1	IBB_MEDSC	P07851 ascaris suu
42	71	14.3	63	1	ICEL_ASCSU	O92832 homo sapien
43	71	14.3	810	1	NEI1_HUMAN	O00174 drosophila
44	71	14.3	3712	1	IMA_DROME	Q41065 pium sativ
45	70.5	14.2	96	1	IBB1_PEA	

ALIGNMENTS

RESULT 1
ID TR17_HUMAN STANDARD; PRT; 184 AA.
AC Q02223;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 17 (B-cell maturation protein).
GN TNFRSF17 OR BCMA OR BCM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A., AND CHROMOSOMAL TRANSLOCATION.
RP TISSUE=Peripheral blood leukocytes, and lymph node;
RC MEDLINE=93010984; PubMed=1396583;
RA Laabi Y., Gras M.P., Carbonnel F., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;
RT "A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a c(4;16)(q26;p13) translocation in a malignant T cell lymphoma.";
RL EMO J. 11:3897-3904(1992).
[2]
RN SEQUENCE FROM N.A.
RX MEDLINE=94218235; PubMed=8165126;
RA Laabi Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;
RT "The BCMA gene, preferentially expressed during B lymphoid maturation, is bidirectionally transcribed.";
RL Nucleic Acids Res. 22:1147-1154(1994).
[3]
RN SEQUENCE FROM N.A.
RX MEDLINE=99425270; PubMed=10493829;
RA Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R., Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L., Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S., Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;
RT "Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";
RL Genomics 60:295-308(1999).
[4]
RN SEQUENCE FROM N.A., AND VARIANT THR-153.
RX MEDLINE=21419161; PubMed=11528522;
RA Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;
RT "Presence of four major haplotypes in human BCMA gene: lack of association with systemic lupus erythematosus and rheumatoid arthritis.";
RL Genes Immun. 2:276-279(2001).
[5]
RN FUNCTION.
RX MEDLINE=20363816; PubMed=10903733;
RA Hatzoglou A., Rousselet J., Bourgeade M.-F., Rogier B., Madry C., Inoue J., Devigne O., Tsapis A.;
RT "TNF receptor family member BCMA (B cell maturation) associates with TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38

RT mitogen-activated protein kinase.";
 RL J. Immunol. 165:1322-1330(2000).
 RP FUNCTION.
 RX MEDLINE=20259066; PubMed=10801128;
 RA Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R.,
 RA Madden K., Xu W., Parrish-Novak J., Foster D., Lofton-Day C.,
 RA Moore W., Little A., Grossman A., Haugen H., Foley K., Blumberg H.,
 RA Harrison K., Kindevogel W., Clegg C.H.,
 RT "TACI and BCMA are receptors for a TNF homologue implicated in B-cell
 RT autoimmune disease.";
 RT Nature 404:995-999(2000).
 RL Nature 404:995-999(2000).
 RN [7]
 RP FUNCTION, AND INTERACTION WITH APRIL AND BAFF.
 RX MEDLINE=21170294; PubMed=10973284;
 RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
 RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
 RA Boyle W.J., Sarsol I., Heu H., Senaldi G., Thell L.E.,
 RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
 RT humoral immunity.";
 RT Nat. Immunol. 1:252-256(2000).
 RL [8]
 RP INTERACTION WITH TRAF5 AND TRAF6.
 RX MEDLINE=20381353; PubMed=10308663;
 RA Shu H.-B., Johnson H.;
 RT "B cell maturation protein is a receptor for the tumor necrosis factor
 RT family member TALL-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).
 CC -1- FUNCTION: Receptor for TNFSF13B/BLYS/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK.
 CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane
 CC and perinuclear Golgi-like structures.
 CC -1- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-
 CC cells or monocytes.
 CC -1- DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS
 CC CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(4;16) (Q26;P13)
 CC WHICH INVOLVES BCMA AND IL2.
 CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
 CC -----
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 CC -----
 CC DR EMBL; 214954; CAA78679.1; -;
 CC DR EMBL; 229575; CAA82691.1; -;
 CC DR EMBL; 229574; CAA82690.1; -;
 CC DR EMBL; U95742; AAB67251.1; -;
 CC DR EMBL; AB052772; BAB60895.1; -;
 CC DR PIR; S31208; S31208.
 CC DR PIR; S31209; S31209.
 CC DR Genew; HGNC:11913; TNFRSF17.
 CC DR MIM; 109545; -;
 CC DR MIM; 109545; -;
 CC KW Receptor; Immune response; Proto-oncogene; Signal-anchor;
 CC Transmembrane; Chromosomal translocation; Polymorphism.
 CC FT DOMAIN 1 54
 CC FT TRANSMEM 55 77
 CC FT SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 CC FT (POTENTIAL).
 CC FT CYTOPLASMIC (POTENTIAL).
 CC FT TNFR-CYS
 CC FT BREAKPOINT FOR TRANSLOCATION TO FORM
 CC FT INTERLEUKIN 2/BCM ONCOGENE.
 CC FT DISULFID 8 21
 CC FT DISULFID 24 37
 CC FT DISULFID 28 41
 CC FT VARIANT 153 153
 CC FT A->T.
 CC FT /FTID=VAR_012234.
 CC SQ SEQUENCE, 184 AA; 20138 MW; 277AF11E2767D932 CRC64;

Query Match 40.4%; Score 201; DB 1; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4,2e-13;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CSQNEFYDSLHACIPCCQRCSSNTPTLCORXC 34
 DB 8 CSQNEFYDSLHACIPCCQRCSSNTPTLCORXC 41
 TR77 MOUSE
 ID TR17 MOUSE STANDARD; PRT; 185 AA.
 AC 088472;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 17 (B-cell
 DE maturation protein).
 DE TNFRSF17 OR BCMA OR BCM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=BALB/c; TISSUE=Spleen;
 RX MEDLINE=99061155; PubMed=9846598;
 RA Madry C., Laabi Y., Callebaut I., Rousset J., Hatzoglou A.,
 RA Le Coniat M., Morion J.P., Berger R., Tsapis A.;
 RT "The characterization of murine BCMA gene defines it as a new member
 RT of the tumor necrosis factor receptor superfamily.";
 RL Int. Immunol. 10:1693-1702(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Akawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamazaki I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schmitt L.M., Stebbins F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barb G.,
 RA Blake J., Boffelli D., Bojunga N., Carinci P., de Bonaldo M.F.,
 RA Brownstein W.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilting L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohcenki S.,
 RA Hayaishiaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -1- FUNCTION: Receptor for TNFSF13B/BLYS/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK (by similarity).
 CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Detected in spleen, thymus, bone marrow and
 CC heart, and at lower levels in kidney and lung.
 CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
 CC -----
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 CC -----
 DR EMBL; AF061505; AAC23799.1; -
 DR EMBL; AK020247; BAB2038.1; -
 DR MGI; MGI:1343050; Tnfra17.
 KW Receptor; Immune response; Signal-anchor; Transmembrane;
 KW Alternative splicing.
 FT DOMAIN 1
 FT TRANSMEM 50
 FT SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT REPEAT 71
 FT 185
 FT BY SIMILARITY.
 FT DISULFID 5
 FT 36
 FT BY SIMILARITY.
 FT DISULFID 21
 FT 32
 FT BY SIMILARITY.
 FT DISULFID 25
 FT 36
 FT MISSING (IN ISOFORM 2).
 FT VARSPLIC 87
 FT 91
 FT 20442 MW; 880635284FD26A8B CRC64;
 FT SEQUENCE 185 AA;
 SO
 Query Match 27.3%; Score 136; DB 1; Length 185;
 Best Local Similarity 70.6%; Pred. No. 8.1e-07;
 Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;
 Qy 1 CSQNEYPDSLHACTPCQLRGSSNTPPTQRCYC 34
 Db 5 CFHSYFDSLHACPKCHLRCSN--PPATCOPYC 36
 RESULT 3
 T13X MOUSE STANDARD; PRT; 249 AA.
 ID T13X MOUSE
 AC Q9ET35; Q9DBZ3;
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
 DE activator and CML interactor).
 GN TNFRSF13B OR TACI.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=21177254; PubMed=10881172;
 RA Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A.,
 RA Dixit V.M.;
 RT "Identification of a receptor for Bly's demonstrates a crucial role in
 RT humoral immunity."
 RT Nat. Immunol. 1:37-41(2000).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Komoto H., Adachi J., Fukuda S.,
 RA Atawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamada S.,
 RA Saito T., Okazaki Y., Gojodori T., Hono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischiemann W., Gasteierland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirral L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Maehiro T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Botfield D., Boujunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guettich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombere P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Saeki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Winking L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,

RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 RN [3]
 RP FUNCTION.
 RX MEDLINE=20341628; PubMed=10880535;
 RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
 RA Theill L.E., Colombero A., Solovayev I., Lee F., McCabe S., Elliott R.,
 RA Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,
 RA Meng S.-Y., Boyle W.J., Hsu H.;
 RT "TRAC1 is a TRAF-interacting receptor for TALL-1, a tumor necrosis
 RT factor family member involved in B cell regulation."
 RL J. Exp. Med. 192:137-143(2000).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=21322748; PubMed=11429548;
 RA Wang H., Marsters S.A., Baker T., Chan B., Lee W.P., Fu L., Tumas D.,
 RA Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.;
 RT "TRAC1-ligand interactions are required for T cell activation and
 RT collagen-induced arthritis in mice."
 RL Nat. Immunol. 2:632-637(2001).
 CC -1- FUNCTION: Receptor for TNFRSF13/APRIL and TNFRSF13B/TALL1/BAFF/BLYS
 CC that binds both ligands with similar high affinity. Mediates
 CC calcineurin-dependent activation of NF-AT, as well as activation
 CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
 CC cell function and the regulation of humoral immunity (by
 CC similarity).
 CC -1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
 CC domain of CMLG with its C-terminus (by similarity).
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
 CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
 CC
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 CC -----
 DR EMBL; AF257673; AAG00081.1; -
 DR EMBL; AK004668; BAB23457.1; -
 DR MGI; MGI:1889411; Tnfra13b.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS50050; TNFR_NGFR_2; 2.
 KW Receptor; Immune response; Signal-anchor; Transmembrane; Repeat.
 FT DOMAIN 1
 FT TRANSMEM 129
 FT SIGNAL-ANCHOR (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT REPEAT 5
 FT 249
 FT BY SIMILARITY.
 FT DISULFID 6
 FT 36
 FT BY SIMILARITY.
 FT DISULFID 22
 FT 34
 FT BY SIMILARITY.
 FT DISULFID 26
 FT 38
 FT BY SIMILARITY.
 FT DISULFID 43
 FT 58
 FT BY SIMILARITY.
 FT DISULFID 61
 FT 72
 FT BY SIMILARITY.
 FT DISULFID 65
 FT 76
 FT BY SIMILARITY.
 FT CONFLICT 137
 FT 137
 FT I -> F (IN REF. 2).
 FT SEQUENCE 249 AA; 26947 MW; CB2F2D61C2931DB1 CRC64;
 SO
 Query Match 19.7%; Score 98; DB 1; Length 249;
 Best Local Similarity 25.6%; Pred. No. 0.0049;
 Matches 23; Conservative 12; Mismatches 27; Indels 28; Gaps 4;
 Qy 1 CSQNEYPDSLHACTPCQLRGSSNTPPTQRCYCCEYFDSLHACPKCHLRCSPPTQRCYC 60
 Db 6 CPKQYDMSRKSVCSCALTCSSGRS-----QRTCTDF-----CKFINCKRKE----- 46
 Qy 61 HSEYFDSLHAC-----PPATCOPYC 81
 Db 47 QGRYYDHLGACVSCDSTCTQHPOCAHFC 76

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RESULT 4
ID T13X_HUMAN STANDARD; PRT; 293 AA.
AC 014836;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
DE activator and CAML interactor).
OS TNFRSF13B OR TACI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA MEDLINE=97458245; PubMed=9311921;
RT von BueLOW G.-U., Bram R.J.;
RT "NF-AT activation induced by a CAML-interacting member of the tumor
RT necrosis factor receptor superfamily.";
RL Science 278:138-141(1997).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Straussberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
[3]
RP FUNCTION.
RA MEDLINE=20519647; PubMed=10956646;
RA Wu Y., Bresette D., Carrell J.A., Kaufman T., Feng P., Taylor K.,
RA Gan Y., Cho Y.H., Garcia A.D., Gollatz E., Dimke D., Lafleur D.,
RA Migone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J.,
RA Olsen H.S., Kanakara P., Moore P.A., Baker K.P.;
RT "Tumor necrosis factor (TNF) receptor superfamily member TACI is a
RT high affinity receptor for TNF family members APRIL and BLys.";
RL J. Biol. Chem. 275:35478-35485(2000).
[4]
RP FUNCTION.
RA MEDLINE=21170294; PubMed=10973284;
RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolima M.,
RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
RT humoral immunity.";
RL Nat. Immunol. 1:252-256(2000).
[5]
RP FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAFF/BLYS
RP that binds both ligands with similar high affinity. Mediates
RP calcineurin-dependent activation of NF-AT, as well as activation
RP of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
RP cell function and the regulation of humoral immunity.
CC -1- SUBUNIT: Binds TRAF2, TRAF3 and TRAF6. Binds the NH2-terminal
CC domain of CAML with its C-terminus.
CC -1- SUBCELLULAR LOCATION: Type III membrane protein.
CC -1- TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small
CC intestine and peripheral blood leukocytes. Expressed in resting B-
CC cells and activated T-cells, but not in resting T-cells.
CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
CC -1- CAUTION: It is uncertain whether Met-1 or Met-31 is the initiator.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF023614; AAC51790.1; -
CC EMBL: BC028072; AAH28072.1; -
CC GenBank: U01815; TNFRSF13B.
CC MIM: 604907; -.

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DR InterPro, IPR001368; TNFR_C6.
DR PROSITE, PS00652; TNFR_NGFR_1; 1.
DR PROSITE, PS50050; TNFR_NGFR_2; FALSE NEG.
KW Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein;
KW Repeat.
FT DOMAIN 1 165 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 166 186 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
FT REPEAT 187 293 CYTOPLASMIC (POTENTIAL).
FT REPEAT 33 67 TNFR-CYS 1.
FT REPEAT 70 104 TNFR-CYS 2.
FT DISULFID 34 47 BY SIMILARITY.
FT DISULFID 50 62 BY SIMILARITY.
FT DISULFID 54 66 BY SIMILARITY.
FT DISULFID 71 86 BY SIMILARITY.
FT DISULFID 89 100 BY SIMILARITY.
FT DISULFID 93 104 BY SIMILARITY.
FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 251 251 P -> L (IN REF. 2).
SQ SEQUENCE 293 AA; 31816 MW; 411799F3DE17A5EB CRC64;

Query Match 18.7%; Score 93; DB 1; Length 293;
Best Local Similarity 28.4%; Pred. No. 0.017;
Matches 21; Conservative 13; Mismatches 22; Indels 18; Gaps 5;

QY 1 CSQNEYFDSLHACIPQGLRCSNTPPLTCORYC-----EYFDSLHACPCLRCS 51
DB 34 CPREGYMPPLLTGTCMSCTICNHQS-QRTCAAFCRSLSCREKGKFDYHLRR--DCISCA 90
QY 52 -----PPTCYCC 59
DB 91 SICGHPKQCAVFC 104

RESULT 5
ID KRUA_HUMAN STANDARD; PRT; 169 AA.
AC P26371;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Keratin, ultra high-sulfur matrix protein A (UHS keratin A) (UHS
DE Kera).
GN KRNI OR UHSK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RP TISSUE=follicle;
RX MEDLINE=9115951; PubMed=1703541;
RA McKinnon P.J., Powell B.C., Rogers G.E.;
RT "Structure and expression of genes for a class of cysteine-rich
RT proteins of the cuticle layers of differentiating wool and hair
RT follicles.";
RL J. Cell Biol. 111:2587-2600(1990).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99148005; PubMed=10023043;
RA Perez C., Auriol J., Gerst C., Bernard B.A., Egly J.-M.;
RT "Genomic organization and promoter characterization of two human UHS
RT keratin genes.";
RL Gene 227:137-148(1999).
[3]
CC -1- FUNCTION: THE KERATIN PRODUCTS OF MAMMALIAN EPIDERMAL DERIVATIVES
CC SUCH AS WOOL AND HAIR CONSIST OF MICROFIBRILS EMBEDDED IN A RIGID
CC MATRIX OF OTHER PROTEINS. THE MATRIX PROTEINS INCLUDE THE HIGH-
CC SULFUR AND HIGH-TYROSINE KERATINS, HAVING MOLECULAR WEIGHTS OF
CC 6-20 kDa, WHEREAS THE MICROFIBRILS CONTAIN THE LARGER, LOW-SULFUR
CC KERATINS (40-56 kDa).
CC -1- TISSUE SPECIFICITY: CUTICLE LAYERS OF DIFFERENTIATING
CC HAIR FOLLICLES.
CC -1- DEVELOPMENTAL STAGE: AT A LATE STAGE OF FIBER DIFFERENTIATION.

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DR SMART, SMO0261; FU, 10.
 DR PROSITE, PS00136; SUBTILASE ASP, 1.
 DR PROSITE, PS00137; SUBTILASE HIS, 1.
 DR PROSITE, PS00138; SUBTILASE SER, 1.
 KW Hydrolyase; Serine protease; Glycoprotein; signal; Transmembrane;
 KW Multigene family; Zymogen; Repeat
 FT SIGNAL 1 319
 FT PROPEP 1 319
 FT CHAIN 320 1680
 FT ACT SITE 418 418
 FT ACT SITE 457 457
 FT ACT SITE 638 638
 FT DOMAIN 962 1444
 FT REPEAT 962 1007
 FT REPEAT 1008 1057
 FT REPEAT 1058 1104
 FT REPEAT 1105 1153
 FT REPEAT 1154 1205
 FT REPEAT 1206 1254
 FT REPEAT 1255 1299
 FT REPEAT 1300 1346
 FT REPEAT 1347 1393
 FT REPEAT 1394 1444
 FT TRANSMEM 1508 1532
 FT DOMAIN 1533 1680
 FT CARBOHYD 3 3
 FT CARBOHYD 109 109
 FT CARBOHYD 130 130
 FT CARBOHYD 203 203
 FT CARBOHYD 443 443
 FT CARBOHYD 481 481
 FT CARBOHYD 928 928
 FT CARBOHYD 1061 1061
 FT CARBOHYD 1182 1182
 FT CARBOHYD 1275 1275
 FT CARBOHYD 1278 1278
 FT CARBOHYD 1440 1440
 SQ SEQUENCE 1680 AA; 183599 MW; 0A99CE8770A8E293 CRC64;
 Query Match 17.5%; Score 87; DB 1; Length 1680;
 Best Local Similarity 25.0%; Pred. No. 0.3; Mismatches 31; Indels 50; Gaps 9;
 Matches 31; Conservative 12; Mismatches 31; Indels 50; Gaps 9;
 QY 1 CSQNEFYDSLHACIPQQRCSNTPLTQ--RYC--CEYFDSLH-----ACP---46
 DB 1051 CPDGYENSRNRTCPVCEBNCAS-----CQHPREYCTSCDH-HLYMHKCYSAACPLDRT 1103
 QY 47 -----CLRCSPPTCYC--CFHSYF--DSLHACPA-----TC 77
 DB 1104 YETEDNKKAFCHSTATCNGPTDQDCITCRSSRYAWQNKCLISCPDGFYADKKRLCEMPC 1163
 QY 78 QPYC 81
 DB 1164 QEGC 1167
 RESULT 8
 PKCS_MOUSE STANDARD; PRT; 1877 AA.
 AC Q04552; Q62040; 01-FEB-1995 (Rel. 31, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Proprotein convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)
 DE (Proprotein convertase PCS5 (Subtilisin/kexin-like protease PCS5
 DE (Convertase PCS5) (PC5) (Subtilisin-like proprotein convertase 6)
 DE (SP66).
 GN PCSK5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCBI_TaxId=10090;
 RN [1]

RP SEQUENCE OF 330-1877 FROM N.A. (ISOFORM PCSB).
 RC STRAIN=ICR; TISSUE=Intestine;
 RX MEDLINE=93327934; PubMed=8335106;
 RA Nakagawa T., Murakami K., Nakayama K.;
 RT "Identification of an isoform with an extremely large Cys-rich region
 RT of PC6, a Kex2-like processing endoprotease.";
 RL PEBB Lett. 327:165-171(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM PCSA).
 RC TISSUE=Brain, and Intestine;
 RX MEDLINE=93224489; PubMed=8468318;
 RA Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K.,
 RA Nakayama K.;
 RT "Identification and functional expression of a new member of the
 RT mammalian Kex2-like processing endoprotease family: its striking
 RT structural similarity to PACE4.";
 RL J. Biochem. 113:132-135(1993).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM PCSA).
 RC TISSUE=Adrenal cortex;
 RX MEDLINE=93342056; PubMed=8341687;
 RA Lusson J., Vileau D., Hamelin J., Day R., Chretien M., Seidah N.G.;
 RT "cDNA structure of the mouse and rat subtilisin/kexin-like PCS5: a
 RT candidate proprotein convertase expressed in endocrine and
 RT nonendocrine cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993).
 RN [4]
 RP PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION.
 RX MEDLINE=97103178; PubMed=8947550;
 RA De Bie I., Marcinkiewicz M., Malide D., Lazure C., Nakayama K.,
 RA Bendayan M., Seidah N.G.;
 RT "The isoforms of proprotein convertase PCS5 are sorted to different
 RT subcellular compartments.";
 RL J. Cell Biol. 135:1261-1275(1996).
 RN [5]
 RP DEVELOPMENTAL EXPRESSION.
 RX MEDLINE=96293359; PubMed=8698813;
 RA Constam D.B., Calton M., Robertson E.J.;
 RT "SPC4, SPC6, and the novel protease SPC7 are coexpressed with bone
 RT morphogenetic proteins at distinct sites during embryogenesis.";
 RL J. Cell Biol. 134:181-191(1996).
 RN [6]
 RP DEVELOPMENTAL EXPRESSION.
 RX MEDLINE=97436919; PubMed=9291583;
 RA Rancourt S.L., Rancourt D.E.;
 RT "Murine subtilisin-like proteasease SPC6 is expressed during embryonic
 RT implantation, somitogenesis, and skeletal formation.";
 RL Dev. Genet. 21:75-81(1997).
 CC -1- FUNCTION: LIKELY TO REPRESENT A WIDESPREAD ENDOPEPTIDASE ACTIVITY
 CC WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE
 CC OF CLEAVAGE AT THE RX (K/R) CONSENSUS MOTIF. MAY BE RESPONSIBLE
 CC FOR THE MATURATION OF GASTROINTESTINAL PEPTIDES. MAY BE INVOLVED
 CC IN THE CELLULAR PROLIFERATION OF ADRENAL CORTEX VIA THE ACTIVATION
 CC OF GROWTH FACTORS.
 CC -1- CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR
 CC PROPROTEINS BY CLEAVAGE OF ARG-XAA-YAA-ARG-|-ZAA BONDS, WHERE XAA
 CC CAN BE ANY AMINO ACID AND YAA IS ARG OR IYS.
 CC -1- SUBCELLULAR LOCATION: PCSA IS SECRETED THROUGH THE REGULATED
 CC SECRETORY PATHWAY. PCSB IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO
 CC A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH
 CC EARLY ENDOSOMES.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS, PCSB/LONG (SHOWN HERE)
 CC AND PCSA/SHORT; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: PCSA IS EXPRESSED IN MOST TISSUES BUT IS MOST
 CC ABUNDANT IN THE TESTES AND ADRENALS. PCSB IS EXPRESSED IN THE
 CC INTESTINE, ADRENALS AND LONG BUT NOT IN THE BRAIN.
 CC -1- DEVELOPMENTAL STAGE: WEAKLY EXPRESSED THROUGHOUT THE EMBRYO,
 CC EXCEPT IN THE DEVELOPING NERVOUS SYSTEM, THE LIVER AND THE LIVER,
 CC BUT MARKEDLY UPREGULATED AT DISCRETE SITES DURING DEVELOPMENT. AT
 CC E6.5, PROMINENT EXPRESSION OBSERVED IN DIFFERENTIATED DECIDUA. AT
 CC E7.5, INTENSE EXPRESSION IN EXTRAEMBRYONIC ENDODERM, AMNION AND
 CC NASCENT MESODERM. AT 8.5, ABUNDANT EXPRESSION IN SOWITES AND YOLK
 CC SAC FOLLOWED BY A CONFINATION TO DERMATOTOME COMPARTMENT. BETWEEN

[illegible]

```

FT CARBOHYD 951 951 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1016 1016 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1220 1220 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1317 1317 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1523 1523 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1711 1711 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1733 1733 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 878 915 GEYIDDHGHCOTGCASCAKCKMGPFOEDCISCPVRYLD -->
FT ATERSMVGGGCMVLKVKNNLCORRVLDQDLCKCTLPQG
FT (IN ISOFORM PCSA).
FT VARSPLIC 916 1877 MISSING (IN ISOFORM PCSA).
SQ SEQUENCE 1877 AA; 209287 MW; ECG50E2DF0EA1C3 CRC64;

Query Match 17.4%; Score 86.5; DB 1; Length 1877;
Best Local Similarity 22.1%; Pred. No. 0.37;
Matches 29; Conservative 6; Mismatches 43; Indels 53; Gaps 3;

OY 1 CSQNEYPDSLHACIPCOLRCSSNTPLTQRCYCEYFDSL----- 42
DB 1481 CAAYVWDEGSHRCOPCHKKSCSGSPEDCCYTPRETFLNTTCVKECBGYHTDKDS 1540
OY 43 -----HACPCLRCSP-----PTQYCCFHSYFDSLHACP----- 73
DB 1541 QOCVCHSSCRRCBEPHMOCLSCRPGVFGKGLLCCRGYIGESISGCEKDKSCK 1600
OY 74 -----PATCQ 78
DB 1601 SCRGPRPTDCQ 1611

RESULT 9
KRA3_SHEEP STANDARD; PRT; 131 AA.
ID P0241;
AC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last annotation update)
DE Keratin, high-sulfur matrix protein, IIA3.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
OC [1]
RN MEDLINE=74022242; PubMed=4584026;
RP SEQUENCE.
RX Swart L.S., Haylett T.;
RA "Studies on the high-sulphur proteins of reduced Merino wool. Amino
RT acid sequence of protein SCMB-3a3";
RL Biochem. J. 133:641-654 (1973).
CC -!- FUNCTION: THE KERATIN PRODUCTS OF MAMMALIAN EPIDERMAL DERIVATIVES
CC SUCH AS WOOL AND HAIR CONSIST OF MICROFILBRILS EMBEDDED IN A RIGID
CC MATRIX OF OTHER PROTEINS. THE MATRIX PROTEINS INCLUDE THE HIGH-
CC SULFUR AND HIGH-TYROSINE KERATINS, HAVING MOLECULAR WEIGHTS OF
CC 6-20 kDa, WHEREAS THE MICROFILBRILS CONTAIN THE LARGER, LOW-SULFUR
CC KERATINS (40-56 kDa).
CC -!- MISCELLANEOUS: THE SOURCE OF THIS PROTEIN IS MERINO WOOL.
CC PIR, A02840; KRHA3.
CC DR InterPro; IPR002494; Keratin_B2.
CC DR Pfam; PF01500; Keratin_B2; I.
SQ SEQUENCE 131 AA; 14163 MW; 8C0B56C0070B1C50 CRC64;

Query Match 16.7%; Score 83; DB 1; Length 131;
Best Local Similarity 25.2%; Pred. No. 0.08;
Matches 26; Conservative 12; Mismatches 35; Indels 30; Gaps 6;

OY 1 CSQNEYPDSLHACIPCOLR---CSNTPPLT-----COR-YCCEYFDSLHA 44
DB 18 CLQPRVYND-----PCCCRPVSCQTVSRPTVFRCTRNPICBERRVCCDPSLGSGC 71
OY 45 CFCILRCSPTCQY-----CCFHSYFDSLHACP---PATCQ 79

```

DB 72 CREDITCPTSCQAVNCRPCWATTCOPUSVQCPCCPTSCOP 114

RESULT 10

UBPW_MOUSE

AC 061068; STANDARD; PRT; 526 AA.

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Ubiquitin carboxyl-terminal hydrolase DUB-1 (EC 3.1.2.15) (Ubiquitin deubiquitinase DUB-1) (Ubiquitin-specific processing protease DUB-1) (Deubiquitinating enzyme 1).

GN DUB1 OR DUB-1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxId=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96194957; PubMed=8622927;

RA Zhu Y., Carroll M., Papa F.R., Hochstrasser M., D'Andrea A.D.;

RT "DUB-1, a deubiquitinating enzyme with growth-suppressing activity.";

RL Proc. Natl. Acad. Sci. U.S.A. 93:3275-3279 (1996).

CC -1- FUNCTION: HAS GROWTH-SUPPRESSING ACTIVITY, INDUCES ARREST IN G1 PHASE UPON CONTROLLED EXPRESSION.

CC -1- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O = ubiquitin + a thiol.

CC -1- INDUCTION: BY INTERLEUKIN-3.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C19.

CC -----

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CC -----

CC DR EMBL; U41636; AAC52532.1; -

DR MEROPS; C19.031; -

DR MGD; MGI:107699; DUB1.

DR InterPro; IPR001394; UCH-2.

DR Pfam; PF00442; UCH-1; 1.

DR Pfam; PF00443; UCH-2; 1.

DR PROSITE; PS00972; UCH_2_1; 1.

DR PROSITE; PS00973; UCH_2_2; 1.

DR PROSITE; PS00395; UCH_2_3; 1.

KW Ubl conjugation pathway; Hydrolase; Thiol protease; Multigene family.

FT ACT_SITE 60 60 BY SIMILARITY.

FT ACT_SITE 298 298 BY SIMILARITY.

FT ACT_SITE 307 307 BY SIMILARITY.

FT ACT_SITE 307 307 BY SIMILARITY.

SO SEQUENCE 526 AA; 59073 MW; 263AA7B579694EA CRC64;

Query Match 16.5%; Score 82; DB 1; Length 526;

Best Local Similarity 35.8%; Pred. No. 0.33;

Matches 19; Conservative 8; Mismatches 18; Indels 8; Gaps 2;

QY 19 LKSSNTPLTCRCYCEYFDSLHACPCRCSPRCYCCCFSEYFDSLHA 71

DB 66 LQCLHTPLPL-----ADYMLSOEHSQTC--CSPEGCKLCAMEALVTOSILHS 110

RESULT 11

LMG3_HUMAN

ID LMG3_HUMAN STANDARD; PRT; 1587 AA.

AC Q9Y6N6;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Laminin gamma-3 chain precursor (laminin 12 gamma 3).

GN LAMC3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxId=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RX MEDLINE=99242614; PubMed=10225960;

RA Koch M., Olson P.F., Albus A., Jin W., Hunter D.D., Brunken W.J.,

RA Burgess R.E., Champlaud M.F.;

RT "Characterization and expression of the laminin gamma3 chain: a novel,

RT non-basement membrane-associated, laminin chain.";

RL J. Cell Biol. 145:605-618 (1999).

CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin is thought to mediate the attachment, migration, and organization of cells into tissues during embryonic development by interacting with other extracellular matrix components.

CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three different polypeptide chains (alpha, beta, gamma), which are bound to each other by disulfide bonds into a cross-shaped molecule comprising one long and three short arms with globules at each end.

CC THE GAMMA-3 CHAIN IS A SUBUNIT OF LAMININ-12.

CC -1- SUBCELLULAR LOCATION: Extracellular.

CC -1- TISSUE SPECIFICITY: Broadly expressed in: skin, heart, lung, and the reproductive tracts.

CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.

CC -1- DOMAIN: DOMAIN IV IS GLOBULAR.

CC -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).

CC -1- SIMILARITY: CONTAINS 1 LAMININ EGF-LIKE DOMAINS.

CC -1- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.

CC -----

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CC -----

CC DR EMBL; AF041835; AAD36991.1; -

DR HSSP; P02468; LTMF.

DR GeneW; HGNC:6494; LAMC3.

DR MIM; 604349; -

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR001886; LamNT.

DR InterPro; IPR000034; Laminin B.

DR InterPro; IPR002049; Laminin_B.

DR Pfam; PF00052; Laminin_B; 1.

DR Pfam; PF00053; Laminin_EGF; 10.

DR Pfam; PF00055; Laminin_Nterm; 1.

DR PRINTS; PR00011; EGF_LAMININ.

DR PRODOM; PD002082; LamNT; 1.

DR PRODOM; PD003031; Laminin_B; 1.

DR SMART; SMO0180; EGF_Lam; 10.

DR SMART; SMO0001; EGF_Like; 1.

DR SMART; SMO0281; LamB; 1.

DR SMART; SMO0136; LamNT; 1.

DR PROSITE; PS00022; EGF_1; 7.

DR PROSITE; PS01186; EGF_2; 2.

DR PROSITE; PS01248; LAMININ_TYPE_EGF; 10.

KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;

KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.

FT SIGNAL 1 19

FT CHAIN 20 1587 LAMININ GAMMA-3 CHAIN.

FT DOMAIN 20 270 LAMININ N-TERMINAL (DOMAIN VII).

FT DOMAIN 271 326 LAMININ EGF-LIKE 1.

FT DOMAIN 327 382 LAMININ EGF-LIKE 2.

FT DOMAIN 383 429 LAMININ EGF-LIKE 3.

FT DOMAIN 430 479 LAMININ EGF-LIKE 4.

FT DOMAIN 480 489 LAMININ EGF-LIKE 5 (N-TERMINAL).

FT DOMAIN 490 672 LAMININ DOMAIN IV.

FT DOMAIN 673 706 LAMININ EGF-LIKE 5 (C-TERMINAL).

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FT DOMAIN 707 754 LAMININ EGF-LIKE 6.
FT DOMAIN 755 809 LAMININ EGF-LIKE 7.
FT DOMAIN 810 865 LAMININ EGF-LIKE 8.
FT DOMAIN 866 916 LAMININ EGF-LIKE 9.
FT DOMAIN 917 964 LAMININ EGF-LIKE 10.
FT DOMAIN 965 1013 LAMININ EGF-LIKE 11.
FT DOMAIN 1014 1057 DOMAIN II AND I.
FT DOMAIN 1071 1141 COILED COIL (POTENTIAL).
FT DOMAIN 1200 1229 COILED COIL (POTENTIAL).
FT DOMAIN 1424 1504 COILED COIL (POTENTIAL).
FT DOMAIN 1535 1579 COILED COIL (POTENTIAL).
FT SITE 1059 1061 CELL ATTACHMENT SITE (POTENTIAL).
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 328 328 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 631 631 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 837 837 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 980 980 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1185 1185 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1518 1518 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1587 AA; 172051 MW; 3CB6B09B5F20319 CRC64;

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Query Match 16.3%; Score 81; DB 1; Length 1587;
Best Local Similarity 31.0%; Pred. No. 1.1;
Matches 22; Conservative 8; Mismatches 31; Indels 10; Gaps 4;

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OY 12 HACICQLRCNSNTPLTCQRYCCEYFDSLHACPCLRC-----SPPTQYCCFHSHEYDPS 67
Db 322 HECLPC--NCSSRSSECTFDR--ELFSTGHCGRCHCRHTAGHCHERCCENFYHWDP 376
OY 68 LHMACPATCQ 78
Db 377 RM-PCQPCDCQ 386

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RESULT 12
PAC4_RAT STANDARD; PRT; 937 AA.
AC 063415;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)

```

```

DB Paired basic amino acid cleaving enzyme 4 precursor (BC 3.4.21.-)
DE (Subtilisin/kexin-like protease PAC4) (Subtilisin-like proprotein
DE convertase 4) (SPC4).
GN PAC4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

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```

RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Hypothalamus, and Pituitary;
RX MEDLINE=94349873; PubMed=8070361;
RA Johnson R.C., Darlington D.N., Hand T.A., Bloomquist B.T., Mains R.E.;
RT "PAC4: a subtilisin-like endoprotease prevalent in the anterior
RT pituitary and regulated by thyroid status.";
RL Endocrinology 135:1178-1185(1994).

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CC -1- FUNCTION: LIKELY TO REPRESENT AN ENDOPEPTASE ACTIVITY WITHIN THE
CC CONSTITUTIVE SECRETORY PATHWAY, WITH UNIQUE RESTRICTED
CC DISTRIBUTION IN BOTH NEUROENDOCRINE AND NON-NEUROENDOCRINE TISSUES
CC AND CAPABLE OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF.
CC -1- CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR
CC PROPEPTERINS BY CLEAVAGE OF ARG-XAA-YAA-ARG-|-ZAA BONDS,
CC WHERE XAA CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
CC -1- COFACTOR: PROBABLY CALCIUM-DEPENDENT (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: HIGH EXPRESSION IN THE ANTERIOR PITUITARY AND
CC IN SEVERAL BRAIN REGIONS, THE ATRIUM, AND THE VENTRICLE.
CC -1- DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
CC ASSISTING THE FOLDING OF THE ZMOGEN WITHIN THE ENDOPLASMIC
CC RETICULUM.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.

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CC -1- SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----

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DR EMBL; L31894; AAA61987.1; -.
DR HSPB; Q99405; IMPT.
DR MEROPS; S08.075; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002174; Furin-like.
DR InterPro; IPR002884; P domain.
DR InterPro; IPR002029; Peptidase_S8.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF01483; P; PARTIAL.
DR PRINTS; PR00723; SUBTILISIN.
DR ProDom; PD000717; P domain; 1.
DR SMART; SM00181; EGF_1.

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DR SMART; SM00261; FU; 5.
DR PROSITE; PS00136; SUBTILASE ASP; 1.
DR PROSITE; PS00137; SUBTILASE HIS; 1.
DR PROSITE; PS00138; SUBTILASE SER; 1.
DR HydroLase; Serine protease; Glycoprotein; Zymogen; Signal; Calcium;
KW Cleavage on pair of basic residues; Repeat.

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FT SIGNAL 1 45
FT PROPEP 46 132
FT CHAIN 133 937
FT FT 4.
FT DOMAIN 133 454 CATALYTIC.
FT FT 477 615 HOMO B.
FT FT 680 937 CYS-RICH MOTIF (CRM) REGION.
FT DOMAIN 132 133 CLEAVAGE (AUTO-).
FT SITE 132 133 CELL ATTACHMENT SITE (POTENTIAL).
FT ACT_SITE 534 536 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 186 186 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 227 227 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 401 401 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 882 882 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 900 900 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 937 AA; 104053 MW; F386557C33705C8 CRC64;

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Query Match 16.2%; Score 80.5; DB 1; Length 937;
Best Local Similarity 24.4%; Pred. No. 0.76;
Matches 30; Conservative 9; Mismatches 39; Indels 45; Gaps 6;

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OY 1 CSQNEYPFSLHACPCLRC-----SNTPPLTCQRYCCEYFDSLHACP----- 46
Db 701 CPLGTFDPTAARRCRCKGCECTGSRSPYOCCLSCRGFTYHOGTNTCVTLCPAGLVAD 760

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OY 47 ----CLRCSPPTCQYC-----CFHSYFDSLHACPATCQ 78
Db 761 SQRCLRGH-PSQCKVDPEKSTVCKEFLARGSCIPDCPEGYFDSLIRC--GECH 817
OY 79 PYC 81
Db 818 HTC 820

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RESULT 13
LMB2_HUMAN STANDARD; PRT; 1798 AA.
AC P55268; Q16321;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)

```

```

DB Laminin beta-2 chain precursor (S-laminin) (Laminin B1s chain).
GN LAMB2 OR LAMS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

CC	Mammalia Eutheria; Primates; Catarrhini; Homidae; Homo.
CC	NCB1_Taxid=9606;
CC	(1)
RP	SEQUENCE FROM N.A.
RX	MEDLINE=95213013; PubMed=7698745;
RA	Mewer U.M., Gerecke D.R., Durkin M.E., Kurtz K.S., Mattei M.-G.,
RA	Champland M.P., Bugeson R.E., Abrecht R.,
RT	"Human beta 2 chain of laminin (formerly S chain): cDNA cloning,
RT	chromosomal localization, and expression in carcinomas.";
RL	Genomics 24:243-252(1994).
CC	(2)
RP	SEQUENCE FROM N.A.
RX	MEDLINE=95316263; PubMed=7795887;
RA	Iivanainen A., Voelkenh R., Salnio K., Eddy R., Shows T.B.,
RA	Saxiola H., Tryggvason K.;
RT	"The human laminin beta 2 chain (S-laminin): structure, expression in
RT	fetal tissues and chromosomal assignment of the LAMB2 gene.";
RL	Matrix Biol. 14:489-497(1995).
CC	-1- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC	is thought to mediate the attachment, migration, and organization
CC	of cells into tissues during embryonic development by interacting
CC	with other extracellular matrix components.
CC	-1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC	different polypeptide chains (alpha, beta, gamma), which are bound
CC	to each other by disulfide bonds into a cross-shaped molecule
CC	comprising one long and three short arms with globules at each
CC	end.
CC	THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4
CC	(S-MEROSIN), AND LAMININ-7 (KS-LAMININ).
CC	-1- SUBCELLULAR LOCATION: Extracellular.
CC	-1- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
CC	COMPONENT). S-LAMININ IS CONCENTRATED IN THE SYNAPTIC
CC	CLEFT OF THE NEUROSCULAR JUNCTION.
CC	-1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
CC	WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC	-1- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.
CC	-1- SIMILARITY: CONTRAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
CC	-1- SIMILARITY: CONTRAINS 12.5 LAMININ EGF-LIKE DOMAINS.
CC	-1- SIMILARITY: CONTRAINS 1 LAMININ DOMAIN IV.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; Z68155; CAA92279.1; -
DR	EMBL; Z68156; CAA92279.1; JOINED.
DR	EMBL; X79683; CAA56130.1; -
DR	EMBL; S77512; AAB34682.2; -
DR	HSSP; P02468; IKLO.
DR	Genew; HGNC:6487; LAMB2.
DR	MIM; 150325; -
DR	InterPro; IPR000561; EGF-like.
DR	InterPro; IPR00186; LamNT.
DR	InterPro; IPR002049; Laminin EGF.
DR	Pfam; PF00053; laminin EGF; 13.
DR	Pfam; PF00055; laminin_Nterm; 1.
DR	PRINTS; PR00011; EGF_LAMININ.
DR	ProDom; PD002082; LamNT; 1.
DR	SMART; SM00180; EGF_Lam; 11.
DR	SMART; SM00136; LamNT; 1.
DR	PROSITE; PS00022; EGF_1; 10.
DR	PROSITE; PS01186; EGF_2; 2.
DR	PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
RW	Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
RW	Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT	SIGNAL 1 32
FT	CHAIN 33 1798 LAMININ BETA-2 CHAIN.
FT	DOMAIN 33 280 LAMININ N-TERMINAL (DOMAIN VI).
FT	DOMAIN 283 346 LAMININ EGF-LIKE 1.

FT	DOMAIN	347	409	LAMININ EGF-LIKE 2.
FT	DOMAIN	410	469	LAMININ EGF-LIKE 3.
FT	DOMAIN	470	521	LAMININ EGF-LIKE 4.
FT	DOMAIN	522	582	LAMININ EGF-LIKE 5. (INCOMPLETE).
FT	DOMAIN	553	781	LAMININ DOMAIN IV.
FT	DOMAIN	783	830	LAMININ EGF-LIKE 6.
FT	DOMAIN	831	876	LAMININ EGF-LIKE 7.
FT	DOMAIN	877	926	LAMININ EGF-LIKE 8.
FT	DOMAIN	927	985	LAMININ EGF-LIKE 9.
FT	DOMAIN	986	1037	LAMININ EGF-LIKE 10.
FT	DOMAIN	1038	1094	LAMININ EGF-LIKE 11.
FT	DOMAIN	1095	1142	LAMININ EGF-LIKE 12.
FT	DOMAIN	1143	1189	LAMININ EGF-LIKE 13.
FT	DOMAIN	1190	1409	DOMAIN 11.
FT	DOMAIN	1410	1442	DOMAIN ALPHA.
FT	DOMAIN	1443	1798	DOMAIN 1.
FT	DOMAIN	1253	1319	COLLED COIL. (POTENTIAL).
FT	DOMAIN	1472	1526	COLLED COIL. (POTENTIAL).
FT	DOMAIN	1577	1790	COLLED COIL. (POTENTIAL).
FT	DISULFID	283	292	BY SIMILARITY.
FT	DISULFID	285	310	BY SIMILARITY.
FT	DISULFID	312	321	BY SIMILARITY.
FT	DISULFID	324	344	BY SIMILARITY.
FT	DISULFID	347	356	BY SIMILARITY.
FT	DISULFID	349	374	BY SIMILARITY.
FT	DISULFID	377	386	BY SIMILARITY.
FT	DISULFID	389	407	BY SIMILARITY.
FT	DISULFID	410	423	BY SIMILARITY.
FT	DISULFID	412	438	BY SIMILARITY.
FT	DISULFID	440	449	BY SIMILARITY.
FT	DISULFID	452	467	BY SIMILARITY.
FT	DISULFID	470	484	BY SIMILARITY.
FT	DISULFID	472	491	BY SIMILARITY.
FT	DISULFID	493	502	BY SIMILARITY.
FT	DISULFID	505	519	BY SIMILARITY.
FT	DISULFID	783	795	BY SIMILARITY.
FT	DISULFID	785	802	BY SIMILARITY.
FT	DISULFID	804	818	BY SIMILARITY.
FT	DISULFID	816	828	BY SIMILARITY.
FT	DISULFID	831	843	BY SIMILARITY.
FT	DISULFID	833	850	BY SIMILARITY.
FT	DISULFID	852	861	BY SIMILARITY.
FT	DISULFID	864	874	BY SIMILARITY.
FT	DISULFID	877	886	BY SIMILARITY.
FT	DISULFID	879	893	BY SIMILARITY.
FT	DISULFID	896	905	BY SIMILARITY.
FT	DISULFID	908	924	BY SIMILARITY.
FT	DISULFID	927	943	BY SIMILARITY.
FT	DISULFID	929	954	BY SIMILARITY.
FT	DISULFID	956	965	BY SIMILARITY.
FT	DISULFID	968	983	BY SIMILARITY.
FT	DISULFID	986	1000	BY SIMILARITY.
FT	DISULFID	988	1007	BY SIMILARITY.
FT	DISULFID	1010	1019	BY SIMILARITY.
FT	DISULFID	1022	1035	BY SIMILARITY.
FT	DISULFID	1095	1107	BY SIMILARITY.
FT	DISULFID	1097	1114	BY SIMILARITY.
FT	DISULFID	1116	1125	BY SIMILARITY.
FT	DISULFID	1128	1140	BY SIMILARITY.
FT	DISULFID	1143	1155	BY SIMILARITY.
FT	DISULFID	1145	1162	BY SIMILARITY.
FT	DISULFID	1164	1173	BY SIMILARITY.
FT	DISULFID	1176	1187	BY SIMILARITY.
FT	DISULFID	1190	1190	BY SIMILARITY.
FT	DISULFID	1193	1193	INTERCHAIN (PROBABLE).
FT	DISULFID	1797	1797	INTERCHAIN (PROBABLE).
FT	CARBOHYD	268	248	INTERCHAIN (PROBABLE).
FT	CARBOHYD	348	368	N-LINKED (GLC/MC. . .)
FT	CARBOHYD	1085	1085	N-LINKED (GLC/MC. . .)
FT	CARBOHYD	1249	1249	N-LINKED (GLC/MC. . .)
FT	CARBOHYD	1308	1308	N-LINKED (GLC/MC. . .)
FT	CARBOHYD	1348	1348	N-LINKED (GLC/MC. . .)
FT	CARBOHYD	1499	1499	N-LINKED (GLC/MC. . .)

FT CONFLICT 914 914 R -> G (IN REF. 2).
 FT CONFLICT 1179 1179 G -> A (IN REF. 2).
 SQ SEQUENCE 1798 AA; 196079 MW; 9555CF5B24850CB7 CRC64;
 Query Match 16.2%; Score 80.5; DB 1; Length 1798;
 Best Local Similarity 26.9%; Pred. No. 1.3;
 Matches 29; Conservative 7; Mismatches 31; Indels 41; Gaps 8;
 QY 1 CSQNEYPDSL- - - - -HACIP- - - - -COL-RCSNTPPLTCORYCC 35
 Db 943 CHQDEYSGQIVCHFRAGYTGRCACAGHFGDPERPGRGQLCSCGNIDPMDD-AC 1000
 QY 36 EYFDSLHACPLNC- - - - -SPTCYC- - - - -CHSEYFDSLHACPPATC 77
 Db 1001 D- - - - -PHTGQCLRLHRTBEPHCHCKPFGQAPARQSCRC- - - - -TC 1040
 RESULT 14
 LMA1_HUMAN STANDARD; PRT; 3075 AA.
 ID LMA1_HUMAN
 AC P25391;
 DT 01-MAY-1992 (Rel. 12, Created)
 DT 01-MAY-1992 (Rel. 12, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Laminin alpha-1 chain precursor (Laminin A chain).
 GN LMA1 OR LAMA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9133420; PubMed=1714537;
 RA Haaparanta T., Uitto J., Ruoslahti E., Engvall E.;
 RT "Molecular cloning of the cDNA encoding human laminin A chain.";
 RL Matrix 11:151-160(1991).
 RN [2]
 RP SEQUENCE OF 1-2628 FROM N.A.
 RX MEDLINE=91264789; PubMed=2049067;
 RA Nishinen M., Vuolteenaho R., Booc-Handford R., Kallunki P.,
 RA Trygvaeson K.;
 RT "Primary structure of the human laminin A chain. Limited expression
 in human tissues.";
 RL Biochem. J. 276:369-379(1991).
 RN [3]
 RP SEQUENCE OF 2397-3072 FROM N.A.
 RX MEDLINE=89280632; PubMed=2733383;
 RA Olsen D., Nagayoshi T., Fazio M., Peltonen J., Jaakkola S.,
 RA Sanborn D., Sasaki T., Kuvantemi H., Chu M.L., Deutzmann R.,
 RA Timpl R., Uitto J.;
 RT "Human laminin: cloning and sequence analysis of cDNAs encoding A, B1
 and B2 chains, and expression of the corresponding genes in human
 skin and cultured cells.";
 RL Lab. Invest. 60:772-782(1989).
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
 is thought to mediate the attachment, migration, and organization
 of cells into tissues during embryonic development by interacting
 with other extracellular matrix components.
 CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 different polypeptide chains (alpha, beta, gamma), which are bound
 to each other by disulfide bonds into a cross-shaped molecule
 comprising one long and three short arms with globules at each
 end.
 CC THE ALPHA-1 CHAIN IS A SUBUNIT OF LAMININ-1 (EHS LAMININ) AND
 CC LAMININ-3 (S-LAMININ).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
 CC COMPONENT).
 CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
 CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
 CC -1- DOMAIN: DOMAINS VI, IV AND G ARE GLOBULAR.
 CC -1- SIMILARITY: CONTAINS 17 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
 CC -1- SIMILARITY: CONTAINS 17 LAMININ EGF-LIKE DOMAINS.

CC -1- SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.
 CC -1- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
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 CC -----
 CC EMBL, X58531, CAA1418.1, -.
 CC F01, S14458, S14458.
 CC DR HSP, Q60675, 1000.
 CC DR Genew, HGNC:6481, LAMA1.
 CC DR MIM, 150320, -.
 CC DR InterPro, IPR000561; EGF-like.
 CC DR InterPro, IPR001886; LAMNT.
 CC DR InterPro, IPR000034; Laminin_B.
 CC DR InterPro, IPR002049; Laminin_EGF.
 CC DR InterPro, IPR001791; Laminin_G.
 CC DR Pfam, PF00052; Laminin_B; 2.
 CC DR Pfam, PF00054; Laminin_EGF; 15.
 CC DR Pfam, PF00055; Laminin_G; 5.
 CC DR Pfam, PF00055; Laminin_Nterm; 1.
 CC DR PRINTS, PR00011, EGF_LAMININ.
 CC DR ProDom, PD002082; LAMNT; 1.
 CC DR ProDom, PD003031; Laminin_B; 2.
 CC DR SMART, SM00180; EGF_Lam; 14.
 CC DR SMART, SM00001; EGF_Like; 1.
 CC DR SMART, SM00281; Lamb; 2.
 CC DR SMART, SM00282; Lamb; 5.
 CC DR SMART, SM00136; LAMNT; 1.
 CC DR PROSITE, PS00022; EGF_1; 11.
 CC DR PROSITE, PS01186; EGF_2; 2.
 CC DR PROSITE, PS01248; LAMININ_TYPR_EGF; 15.
 CC DR PROSITE, PS50025; LAM_G_DOMAIN; 5.
 CC KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
 CC Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
 CC FT SIGNAL 1 17
 CC FT CHAIN 18 3075
 CC FT DOMAIN 18 269 LAMININ N-TERMINAL (DOMAIN VI).
 CC FT DOMAIN 270 326 LAMININ EGF-LIKE 1.
 CC FT DOMAIN 327 396 LAMININ EGF-LIKE 2.
 CC FT DOMAIN 397 453 LAMININ EGF-LIKE 3.
 CC FT DOMAIN 454 502 LAMININ EGF-LIKE 4.
 CC FT DOMAIN 503 512 LAMININ EGF-LIKE 5 (N-TERMINAL).
 CC FT DOMAIN 517 708 LAMININ DOMAIN IV 1 (DOMAIN IV B).
 CC FT DOMAIN 709 741 LAMININ EGF-LIKE 6.
 CC FT DOMAIN 742 790 LAMININ EGF-LIKE 7.
 CC FT DOMAIN 791 848 LAMININ EGF-LIKE 8.
 CC FT DOMAIN 849 901 LAMININ EGF-LIKE 9.
 CC FT DOMAIN 902 950 LAMININ EGF-LIKE 10.
 CC FT DOMAIN 951 997 LAMININ EGF-LIKE 11.
 CC FT DOMAIN 998 1043 LAMININ EGF-LIKE 12.
 CC FT DOMAIN 1044 1089 LAMININ EGF-LIKE 13.
 CC FT DOMAIN 1090 1149 LAMININ EGF-LIKE 14 (N-TERMINAL).
 CC FT DOMAIN 1150 1159 LAMININ EGF-LIKE 15.
 CC FT DOMAIN 1160 1361 LAMININ DOMAIN IV 2 (DOMAIN IV A).
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Page 13

FT	REPEAT	611	644	7.
SQ	SEQUENCE	965 AA;	108494 MW;	121C57BB07C6FA9D CRC64;

Query Match	16.0%;	Score 79.5;	DB 1;	Length 965;
Best Local Similarity	29.6%;	Pred. No. 0.98;		
Matches 29; Conservative	6;	Mismatches 26;	Indels 37;	Gaps 7;

QY 12 HACT-PCQLACSSWTPPTLTQRYC-----CEYFDSLHAACPC-----LRCSB-P 53
 Db 456 HICLKPCNLTLTSCGHH--KCGRKCHPGKCPCLCESDSNDLVCPGNTVVPAPVRCCGTLKP 513

QY	54	TCQYCCF-----	HSEYFDSLHACPPAT	76
		:	:	
Db	514	TCNHPCIKVVGESTCGHKMPHTCH--	SLDVSCPCT	549

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Search completed: February 4, 2003, 12:58:09
Job time : 8.5749 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 4, 2003, 12:56:21 / Search time 9.51012 Seconds
(without alignments)
818.800 Million cell updates/sec

Title: US-09-854-864-13

Perfect score: 498

Sequence: 1 CSQNEYFDSLHACIPCOLR.....SEYFDSLHACPPATCPQRYC 81

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	201	40.4	184	2 S43486	B-cell maturation
2	94.5	19.0	223	2 B38346	ultra-high-sulfur
3	94.5	19.0	230	2 A38346	ultra-high-sulfur
4	92.5	18.6	169	1 S18946	ultra-high-sulfur
5	91.5	18.4	186	2 A45910	ultra-high-sulfur
6	89	17.9	1574	2 T13954	MEGF6 protein - ra
7	87	17.5	1680	2 A43434	furin (EC 3.4.21.7
8	86.5	17.4	1548	2 S34583	serine proteinase
9	86	17.3	188	2 JG6547	high sulfur protei
10	83	16.7	131	1 KRSH3	keratin high-sulfu
11	83	16.7	175	2 S37649	high-sulfur kerati
12	82	16.5	126	2 I46489	cysteine-rich hair
13	82	16.5	526	2 JG6133	deubiquitinating e
14	81	16.3	2823	2 T23064	hypothetical prote
15	81	16.3	2823	2 F87908	protein T22A3.8 (i
16	81	16.3	3102	2 T43291	laminin alpha chai
17	80.5	16.2	151	2 S60314	hair keratin cyste
18	80.5	16.2	937	2 I53282	gene PACE4 protein
19	80.5	16.2	1101	2 T16840	hypothetical prote
20	80.5	16.2	1798	2 S53869	laminin beta-2 cha
21	80	16.1	3075	2 S14458	laminin alpha-1 ch
22	79.5	16.0	965	2 S62935	hypothetical prote
23	79.5	16.0	1077	2 T41146	probable cysteine-
24	79.5	16.0	3133	2 S52093	hemocytin - silkw
25	79	15.9	861	2 A48825	Norch homolog Mocr
26	78.5	15.8	201	2 D71190	hypothetical prote
27	78.5	15.8	294	2 T23682	hypothetical prote
28	78	15.7	572	2 T29880	hypothetical prote
29	78	15.7	1188	2 D86236	protein F14N23.5 (

30	77.5	15.6	132	1 KRGT3J	keratin high-sulfu
31	77.5	15.6	177	2 S37650	high-sulfur kerati
32	77	15.5	162	2 I47107	high-sulfur wool m
33	77	15.5	172	1 KRSH3	keratin high-sulfu
34	77	15.5	5376	2 T42215	zonadhesin - mouse
35	76.5	15.4	932	2 I52527	PACE4A - mouse (fr
36	76.5	15.4	1513	2 T23681	hypothetical prote
37	76.5	15.4	2414	2 A54277	transcription adap
38	76	15.3	172	2 I47106	high-sulfur wool m
39	76	15.3	182	2 I47105	high-sulfur wool m
40	76	15.3	1299	2 T43251	furin (EC 3.4.21.7
41	76	15.3	2440	2 S39162	transcription coac
42	76	15.3	2441	2 S39161	CRBP-binding prote
43	76	15.3	2910	2 T42214	ocogelin - mouse
44	75.5	15.2	654	2 T30136	hypothetical prote
45	75.5	15.2	1713	2 A55347	adhesive ligand ep

ALIGNMENTS

RESULT 1
S43486
B-cell maturation factor - human
N:Alternate names: BCM protein; BCM protein; BCL protein
C:Species: Homo sapiens (man)
C>Date: 27-Jan-1995 #sequence revision 27-Jan-1995 #text_change 21-Jul-2000
C:Accession: S43486; S31208; S35661
R:Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
Nucleic Acids Res. 22, 1147-1154, 1994
A>Title: The BCM gene, preferentially expressed during B lymphoid maturation, is bidire
A:Reference number: S43486; MUID:94218235; PMID:8165126
A:Accession: S43486
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-184 <LAA>
A:Cross-references: EMBL:Z14954; NID:G29407; PIDN:CA478679.1; PID:G29408
A:Accession: S31208
A:Molecule type: mRNA
A:Residues: 1-184 <LAA>
A:Cross-references: EMBL:Z14955
C:Genetics:
A:Gene: GDB:BCM
A:Cross-references: GDB:135977; OMIM:109545
A:Map position: 16p13.1-16p13.1
A:Introns: 44/1; 93/1
C:Superfamily: human B-cell maturation factor

Query Match 40.4%; Score 201; DB 2; Length 184;
Best local Similarity 100.0%; Pred. No. 8.1e-11;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSTNPPLTCORYC 34
DB 8 CSQNEYFDSLHACIPCOLRCSSTNPPLTCORYC 41

RESULT 2
B38346
ultra-high-sulfur keratin 2 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 24-Sep-1999
C:Accession: A38600; B38346
R:Wood, L.; Mills, M.; Hatzebuhler, N.; Vogeli, G.

J. Biol. Chem. 266, 4024, 1991
A>Title: Serine-rich ultra high sulfur protein gene expression in murine hair and skin
A/Reference number: A38660; MUID:9154184; PMID:1840598
A/Accession: A38660
A/Molecule type: DNA
A/Residues: 1-223 <MO2>
A/Cross-references: GB:M37760; NID:G200963; PIDN:AAA40107.1; PID:G200964
A/Note: This is a correction
R/Wood, L.; Mills, M.; Hatzenbuehler, N.; Vogel, G.
J. Biol. Chem. 265, 21375-21380, 1990
A>Title: Serine-rich ultra high sulfur protein gene expression in murine hair and skin
A/Reference number: A38346; MUID:91065960; PMID:2250030
A/Accession: B38346
A/Molecule type: DNA
A/Residues: 1-21, 'GGCGSGCGCGCGSGCGSCCKPCVC', 22-40, 'GSG', 44-45, 'G', 47-48, 'S', 50, 'GSS',
<MOO>
A/Cross-references: GB:M37759; NID:G200961; PIDN:AAA40106.1; PID:G200962
A/Note: the sequence reported in this paper has been corrected. See A38660
C/Superfamily: ultra-high-sulfur keratin

Query Match 19.0%; Score 94.5; DB 2; Length 223;
Best Local Similarity 29.6%; Pred. No. 0.15;
Matches 24; Conservative 3; Mismatches 27; Indels 27; Gaps 5;

QY 1 CSQNEYFDSLHACIPQALRCSSNTPTLCQRYCCYFDSLHACPLRCSPPTCCYCCF 60
DB 150 CCQSS-----CCKPC---CSCGCGSSCCQSSCCK-----PCC-CQSSCCKPCC 189

QY 61 HSEYFDSLHACPPATQPYC 81
DB 190 QSS-----CCKPCCQSSC 203

RESULT 3
A38346
ultra-high-sulfur keratin 1 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 24-Sep-1999
C/Accession: A38346
R/Wood, L.; Mills, M.; Hatzenbuehler, N.; Vogel, G.
J. Biol. Chem. 265, 21375-21380, 1990
A>Title: Serine-rich ultra high sulfur protein gene expression in murine hair and skin
A/Reference number: A38346; MUID:91065960; PMID:2250030
A/Accession: A38346
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-230 <MOO>
A/Cross-references: GB:M37759; NID:G200961; PIDN:AAA40106.1; PID:G200962
C/Superfamily: ultra-high-sulfur keratin

Query Match 19.0%; Score 94.5; DB 2; Length 230;
Best Local Similarity 29.6%; Pred. No. 0.15;
Matches 24; Conservative 3; Mismatches 27; Indels 27; Gaps 5;

QY 1 CSQNEYFDSLHACIPQALRCSSNTPTLCQRYCCYFDSLHACPLRCSPPTCCYCCF 60
DB 149 CCQSS-----CCKPC---CSCGCGSSCCQSSCCK-----PCC-CQSSCCKPCC 188

QY 61 HSEYFDSLHACPPATQPYC 81
DB 189 QSS-----CCKPCCQSSC 202

RESULT 4
S18946
ultra high-sulfur keratin 1 - human
N/Alternate names: UHS keratin; ultra high-sulfur matrix protein
C/Species: Homo sapiens (man)
C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C/Accession: S18946; B36686
R/Draheit, B.; Doenecke, D.
Submitted to the EMBL Data Library, December 1991
A/Description: Nucleotide sequence of a Human high-sulfur keratin cDNA.

A/Reference number: S18946
A/Accession: S18946
A/Molecule type: mRNA
A/Residues: 1-169 <DRA>
A/Cross-references: EMBL:X63755; NID:G32471; PIDN:CAA45283.1; PID:G32472
R/Mackinnon, P.J.; Powell, B.C.; Rogers, G.E.
J. Cell Biol. 111, 2587-2600, 1990
A>Title: Structure and expression of genes for a class of cysteine-rich proteins of the
A/Reference number: A36686; MUID:91115951; PMID:1703541
A/Accession: B36686
A/Molecule type: DNA
A/Residues: 1-39, 'Y', 41-169 <MAC>
A/Cross-references: GB:X55293; NID:G34078; PIDN:CAA39005.1; PID:G34079
C/Genetics:
A/Genes: GDB:KRN1
A/Cross-references: GDB:125257; OMIM:148021
A/Map position: 11q13-11q13
C/Superfamily: ultra-high-sulfur keratin
C/Keywords: hair; tandem repeat
F/7-15/Region: Ser-rich nonapeptide repeat
F/59-68/Region: Gly-rich decapeptide repeat
F/69-78/Region: Gly-rich decapeptide repeat
F/79-88/Region: Cys-rich decapeptide repeat
F/89-97/Region: Ser-rich nonapeptide repeat
F/98-107/Region: Cys-rich decapeptide repeat
F/108-117/Region: Cys-rich decapeptide repeat
F/118-126/Region: Ser-rich nonapeptide repeat
F/127-136/Region: Cys-rich decapeptide repeat
F/137-145/Region: Ser-rich nonapeptide repeat
F/146-155/Region: Cys-rich decapeptide repeat
F/156-165/Region: Cys-rich decapeptide repeat

Query Match 18.6%; Score 92.5; DB 1; Length 169;
Best Local Similarity 30.0%; Pred. No. 0.18;
Matches 27; Conservative 5; Mismatches 37; Indels 21; Gaps 5;

QY 1 CSQNEYFDSLHACIPQALRCSSNTPTLCQRYCCYFDSLHACPLRCSPPTCCYCCF 51
DB 77 CSQ-----CCKPC---CSCGCGSSCCQSSCCKPCPCSSGSGSSCCQ 127

QY 52 PPTCCYCCFHSYFDSLHACPPATQPYC 81
DB 128 SSCCKPCCSSGCGSS---CQSSCCKPCC 154

RESULT 5
A45910
ultra-high-sulfur keratin - mouse
C/Species: Mus musculus (house mouse)
C/Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 24-Sep-1999
C/Accession: A45910
R/McNabb, A.R.; Wood, L.; Thieriault, N.; Giernan, T.; Vogel, G.
J. Invest. Dermatol. 92, 263-266, 1989
A>Title: An ultra-high sulfur keratin gene is expressed specifically during hair growth.
A/Reference number: A45910; MUID:89140394; PMID:2463353
A/Accession: A45910
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-186 <MCN>
A/Cross-references: GB:M27665; NID:G341749; PIDN:AAA81560.1; PID:G1066818
C/Superfamily: ultra-high-sulfur keratin

Query Match 18.4%; Score 91.5; DB 2; Length 186;
Best Local Similarity 34.7%; Pred. No. 0.24;
Matches 25; Conservative 4; Mismatches 24; Indels 19; Gaps 6;

QY 14 CTP-CQLRC--SSNTPTLCQRYCCYFDSLHACPLRCSPPTCCYCCFHSYFDSL 69
DB 85 CQPCQPCSCGSSCCQPCPCSSCCQPCPCSSCCQPC---CPSCCQSSC----- 132

QY 70 HACPPATQPYC 81
DB 133 --CRPC-CQPC 141

A:Experimental source: clone T22A3

C:Genetics:

A:Gene: CESP:T22A3.8

A:Map position: 1

A:Introns: 45/1; 282/2; 312/3; 416/2; 1255/3; 1329/3; 1418/3; 1776/2; 1988/2; 2760/2

C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h

Query Match 16.3%; Score 81; DB 2; Length 2823;

Best Local Similarity 27.7%; Pred. No. 14;

Matches 26; Conservative 10; Mismatches 32; Indels 26; Gaps 7;

Qy 1 CSQNEYFDSLHACIPCOLRCSSNPPL---TCQRYCCYFDSLHACPLRC-----SPP 53

Db 873 CSDGFEDPLGKCIETC--TCGNIDPMGIGNC-----DS--ETGKCLKICIGHTGD 920

Qy 54 TCQYCCFHSEYFDSLHACPPATC-----QPYC 81

Db 921 SCESCKEH-HWGNAQLHTCKPCGCHTQGA VNPQC 953

RESULT 15

F87908

protein T22A3.8 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-Aug-2001

C:Accession: F87908; E87908

R:anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog

A:Reference number: A75000; MUID:93069613; PMID:9851916

A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_ele

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: F87908

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-2823 <STO>

A:Cross-references: GB:chr_I; PIDN:CAA15432.1; PID:g3924779; GSPDB:GN00019; CESP:T22A3.8

A:Accession: E87908

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-2823 <ST2>

A:Cross-references: GB:chr_I; PIDN:CAB03385.1; PID:g3924881; GSPDB:GN00019; CESP:T22A3.8

C:Genetics:

A:Gene: T22A3.8

A:Map position: 1

C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h

Query Match 16.3%; Score 81; DB 2; Length 2823;

Best Local Similarity 27.7%; Pred. No. 14;

Matches 26; Conservative 10; Mismatches 32; Indels 26; Gaps 7;

Qy 1 CSQNEYFDSLHACIPCOLRCSSNPPL---TCQRYCCYFDSLHACPLRC-----SPP 53

Db 873 CSDGFEDPLGKCIETC--TCGNIDPMGIGNC-----DS--ETGKCLKICIGHTGD 920

Qy 54 TCQYCCFHSEYFDSLHACPPATC-----QPYC 81

Db 921 SCESCKEH-HWGNAQLHTCKPCGCHTQGA VNPQC 953

Search completed: February 4, 2003, 12:59:45

Job time : 12.5101 secs

RESULT 6

T13954
MEGF6 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C:Accession: T13954
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A:Reference number: 214126; MUID:98360089; PMID:9693030
A:Accession: T13954
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1574 <NAK>
A:Cross-references: EMBL:AB011532; NID:G3449293; PIDN:BAA32462.1; PID:G3449294
A:Experimental source: strain Sprague-Dawley; brain
C:Genetics:
A:Gene: MEGF6

Query Match 17.9%; Score 89; DB 2; Length 1574;
Best Local Similarity 29.4%; Pred. No. 1.8;
Matches 30; Conservative 9; Mismatches 25; Indels 38; Gaps 8;

Qy 1 CSONEYFDSLHACIPCOL-----RCSNTPLT-----CQRYCCEY-----FDSLHACPC 47

Db 966 CSAGAPCDAVTGSCI-CPAGRWPRCAQSCPLTFGLNCSQICTCFNGASCDSVTGQC-- 1022

Qy 48 LRCSF-----PTQVCCCFHSEYFDSLHACPPA-----TCQPYC 81

Db 1023 -HCAPGMWGPTC-----LQACPPGLYKNCQHSK 1050

RESULT 7

A43434
furin (EC 3.4.21.75) 2 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Mar-2000
C:Accession: A43434
R:Roebroek, A.J.; Creemers, J.W.; Pauli, I.G.; Kurzik-Dumke, U.; Rentrop, M.; Gateff, E.
J. Biol. Chem. 267, 17208-17215, 1992
A:Title: Cloning and functional expression of Dfurin2, a subtilisin-like proprotein proc
A:Reference number: A43434; MUID:92381036; PMID:1512259
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1680 <ROE>
A:Cross-references: GB:M94375; NID:G157461; PID:G157462
A:Note: sequence extracted from NCBI backbone (NCBIN:111933, NCBIP:111934)
C:Genetics:
A:Gene: FlyBase:Fur2
A:Cross-references: FlyBase:FBgn0004598
C:Superfamily: subtilisin homology
C:Keywords: hydrolase; serine proteinase; transmembrane protein
F:409-652/Domain: subtilisin homology <SBT>
F:418,657,638/Active site: Asp, His, Ser #status predicted

Query Match 17.5%; Score 87; DB 2; Length 1680;
Best Local Similarity 25.0%; Pred. No. 2.9;
Matches 31; Conservative 12; Mismatches 31; Indels 50; Gaps 9;

Qy 1 CSONEYFDSLHACIPCOLRCSNTPLTQC---RYC---CEYFDSLH-----ACP--- 46

Db 1051 CPDGFENSRNRTVCPCPNCAS-----CQHPFYCTSCDH-HLVVHEHKCYACPLDT 1103

Qy 47 -----CLRCSPTCQVC---CFHSEYF---DSLHACPPA-----TC 77

Db 1104 YETEDNKAFCCHCATCNGPTDQDCITCRSSRYAWQNKCLISCPDGFYADKKLECMPC 1163

Qy 78 QPYC 81

Db 1164 QEGC 1167

RESULT 8

S34583
serine proteinase (EC 3.4.21.-) PC6B - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C:Accession: S34583
R:Nakagawa, T.; Murakami, K.; Nakayama, K.
FEBS Lett. 327, 165-171, 1993
A:Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a
A:Reference number: S34583; MUID:93327934; PMID:8335106
A:Accession: S34583
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1548 <NAK>
A:Cross-references: GB:D17583; NID:G407344; PIDN:BAA04507.1; PID:dl005033; PID:G440374
C:Keywords: hydrolase; serine proteinase

Query Match 17.4%; Score 86.5; DB 2; Length 1548;
Best Local Similarity 22.1%; Pred. No. 3;
Matches 29; Conservative 6; Mismatches 43; Indels 53; Gaps 3;

Qy 1 CSONEYFDSLHACIPCOLRCSNTPLTQCRCYCEYFDSL----- 42

Db 1152 CAAVEYDEGSHRCQPCCHKKSCGSPSEDQCYTCPRFTLLNTTCVKECEGYYHTDKDS 1211

Qy 43 -----HACPCLCRSP-----PTQVCCCFHSEYFDSLHACP----- 73

Db 1312 QCVLCHSSCRTCEGPHSMQCLSCRPGWFLGKELLCQCRDGYGTESTGRCEKCKSK 1271

Qy 74 -----PATCQ 78

Db 1272 SCGRPRPTDQ 1282

RESULT 9

JC6547
high sulfur protein B2E - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jul-2000
C:Accession: JC6547
R:Mitsui, S.; Ohuchi, A.; Adachi-Yamada, T.; Hotta, M.; Taubpi, R.; Ogawa, H.
Gene 208, 123-129, 1998
A:Title: Structure and hair follicle-specific expression of genes encoding the rat high
A:Reference number: JC6547; MUID:98201605; PMID:9524245
A:Accession: JC6547
A:Molecule type: DNA
A:Residues: 1-188 <MIT>
A:Cross-references: DDBJ:AB003753; NID:G3046870; PIDN:BAA25573.1; PID:G3046871
C:Comment: This protein is a cysteine-rich, keratin associated protein.
C:Genetics:
A:Gene: b2E
C:Superfamily: keratin high-sulfur matrix protein IIIA
C:Keywords: hair

Query Match 17.3%; Score 86; DB 2; Length 188;
Best Local Similarity 22.5%; Pred. No. 0.73;
Matches 29; Conservative 10; Mismatches 28; Indels 62; Gaps 7;

Qy 1 CSONEYFDSLHACIP-----CQLRCSNTPLTQC-----R 32

Db 69 CSQSS-----CCQPSCCQTCQPTCCQNS---SCQSCCGTSGSGSGSGATSCVR 118

Qy 33 YC---CEYFDSLHACCLRCSPPTC-----YCCFHSYFDSLHAC 72

Db 119 WCRPDCRVEGTCLPPCCVWSCTPTCCQLHHAQASCCRPSCYCGQSCCRPA-----CCCHCC 174

Qy 73 PPATCQPYC 81

Db 175 EPSCSKPSC 183

RESULT 10
KSH3A3
keratin high-sulfur matrix protein IIIA3 - sheep
N:Alternate names: M2.6 protein
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 16-Aug-1996
C:Accession: A02840
R:Swart, L.S.; Haylett, T.
Biochem. J. 133, 641-654, 1973
A>Title: Studies on the high-sulfur proteins of reduced merino wool. Amino acid sequence
A:Reference number: A90269; MUID:74022242; PMID:4584026
A:Molecule type: protein
A:Residues: 1-131 <SWA>
A:Experimental source: Merino wool
C:Comment: Wool and hair consist of microfibrils embedded in a rigid matrix of other proteins
C:Superfamily: keratin high-sulfur matrix protein IIIA
C:Keywords: duplication; hair

Query Match 16.7%; Score 83; DB 1; Length 131;
Best Local Similarity 25.2%; Pred. No. 1;
Matches 26; Conservative 12; Mismatches 35; Indels 30; Gaps 6;

QY 1 CSQNEYFDSLHACIPQLR---CSSNTPLT-----COR-YCCYFDSLHLHA 44
DB 18 CLQPRYRD-----PCCRPVSCQVSRPVTFVPRCTRPICPCRRPVCCDPCSLQEGC 71
QY 45 CPCLRCSPPTCQY-----CCFHSEYFDSLHACP---PATCQP 79
DB 72 CRPTCCPTSCQAVGRCPCWATTCQPVSVQPCRCRPTSCQP 114

RESULT 11
S37649
high-sulfur keratin - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
R:Zhunabeva, B.D.; Gening, L.V.; Gazaryan, K.G.
Mol. Biol. 26, 550-555, 1992
A>Title: Cloning and structural characterization of human hair sulfur-rich keratin genes
A:Reference number: S37649
A:Accession: S37649
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-175 <ZHU>
A:Cross-references: EMBL:X63338; NID:G311881; PIDN:CAA44938.1; PID:G311882
C:Superfamily: keratin high-sulfur matrix protein IIIA

Query Match 16.7%; Score 83; DB 2; Length 175;
Best Local Similarity 32.4%; Pred. No. 1.3;
Matches 22; Conservative 6; Mismatches 24; Indels 16; Gaps 5;

QY 17 CQLRCSSNTPLTCQRYCCYFDSLHACPLRCSPPTCQ--YCCF-HSEYFDSLHACP 73
DB 25 CQPSCCETS---CCQPSCE-----TSC-----CQPSCCQTSFCDLQSLVQLSQQ 71
QY 74 PATCQPYC 81
DB 72 PSCCETSC 79

RESULT 12
I46489
cysteine-rich hair keratin associated protein - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 24-Sep-1999
C:Accession: I46489; S49201
R:Powell, B.C.; Arthur, J.; Nesci, A.
Differentiation 58, 227-232, 1995
A>Title: Characterization of a gene encoding a cysteine-rich keratin associated protein
A:Reference number: I46489; MUID:95228955; PMID:7536172
A:Accession: I46489

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-126 <POW>

A:Cross-references: EMBL:X80035; NID:G510540; PIDN:CAA56339.1; PID:G510541

C:Genetics:

C:Gene: KAP4L

C:Superfamily: ultra-high-sulfur keratin

Query Match 16.5%; Score 82; DB 2; Length 126;

Best Local Similarity 30.3%; Pred. No. 1.2;

Matches 23; Conservative 6; Mismatches 23; Indels 24; Gaps 6;

QY 14 CIP--CQLRCSSNTPLTCQRYCCYFDSLHACPLRCSPPTCQ-----YCCFHSEYF 65

DB 26 CRPSCCRPQCCQ---PSCCRPTCC-----ISSC-----CRPQCCSVCCQPCRCRPSCVI 72

QY 66 DSLHLHACPPATCQPYC 81

DB 73 SS---CCRPTCCRPTC 85

RESULT 13

JC6133

deubiquitinating enzyme - mouse

N:Alternate names: DUB-1 protein

C:Species: Mus musculus (house mouse)

C>Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 05-Nov-1999

C:Accession: JC6133

R:Zhu, Y.; Carroll, M.; Papa, F.R.; Hochstrasser, M.; D'Andrea, A.D.

Proc. Natl. Acad. Sci. U.S.A. 93, 3275-3279, 1996

A>Title: DUB-1, a deubiquitinating enzyme with growth-suppressing activity.

A:Reference number: JC6133; MUID:96194957; PMID:8622927

A:Accession: JC6133

A:Molecule type: mRNA

A:Residues: 1-526 <ZHU>

A:Cross-references: GB:U41636; NID:G1302629; PIDN:ACS2532.1; PID:G1302630

C:Comment: This enzyme is the first enzyme of the ubiquitin system directly implicated

and cell cycle progression, and in cytokine-induced cell proliferation.

C:Genetics:

A:Gene: dub-1

Query Match 16.5%; Score 82; DB 2; Length 526;

Best Local Similarity 35.8%; Pred. No. 3.4;

Matches 19; Conservative 8; Mismatches 18; Indels 8; Gaps 2;

QY 19 LRCSNTPLTCQRYCCYFDSLHACPLRCSPPTCQYCCFHSEYFDSLHLA 71

DB 66 LQCLHTHTPL-----ADYMLSQEHSQTC--CSPEGCKLCAMEALVTQSLHS 110

RESULT 14

T23064

hypothetical protein T22A3.8 - Caenorhabditis elegans (fragment)

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000

C:Accession: T23064; T25096

R:Barlow, K.

submitted to the EMBL Data Library, October 1997

A:Reference number: Z19669

A:Accession: T23064

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-2823 <WIL>

A:Cross-references: EMBL:AL008585; PIDN:CAA15432.1; GSPDB:GN00019; CESP:T22A3.8

A:Experimental source: clone H10E24

R:McMurray, A.

submitted to the EMBL Data Library, October 1996

A:Reference number: Z19980

A:Accession: T25096

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-2823 <W12>

A:Cross-references: EMBL:Z81125; PIDN:CAB03385.1; GSPDB:GN00019; CESP:T22A3.8